

SEQUENCE LISTING

<110> Croteau, Rodney B
Bohlmann, Joerg
Steele, Christopher L
Phillips, Michael A

<120> MONOTERPENE SYNTHASES FROM GRAND FIR (ABIES GRANDIS)

<130> WSUR18414

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<150> 09/360,545
<151> 1999-07-26

<150> 60/052,249
<151> 1997-07-11

<150> PCT/US98/14528
<151> 1998-07-10

<160> 107

<170> PatentIn Ver. 2.0

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<222> (69)..(1952)
<223> Clone AG2.2 encoding myrcene synthase

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Met Ala Val Ser Ile Ser Pro Leu Ala Ser Lys Ser Cys
1 5 10

ctg cgc aag tcg ttg atc agt tca att cat gaa cat aag cct ccc tat 158
Leu Arg Lys Ser Leu Ile Ser Ser Ile His Glu His Lys Pro Pro Tyr
15 20 25 30

aga aca atc cca aat ctt gga atg cgt agg cga ggg aaa tct gtc acg 206
Arg Thr Ile Pro Asn Leu Gly Met Arg Arg Arg Gly Lys Ser Val Thr
35 40 45

cct tcc atg agc atc agt ttg gcc acc gct gca cct gat gat ggt gta 254
Pro Ser Met Ser Ile Ser Leu Ala Thr Ala Ala Pro Asp Asp Gly Val
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caa aga cgc ata ggt gac tac cat tcc aat atc tgg gac gat gat ttc 302
Gln Arg Arg Ile Gly Asp Tyr His Ser Asn Ile Trp Asp Asp Asp Phe
65 70 75

ata cag tct cta tca acg cct tat ggg gaa ccc tct tac cag gaa cgt 350

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gct	gag	aga	tta	att	gtg	gag	gta	aag	aag	ata	ttc	aat	tca	atg	tac	398
Ala	Glu	Arg	Leu	Ile	Val	Glu	Val	Lys	Lys	Ile	Phe	Asn	Ser	Met	Tyr	
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ctg	gat	gat	gga	aga	tta	atg	agt	tcc	ttt	aat	gat	ctc	atg	caa	cgc	446
Leu	Asp	Asp	Gly	Arg	Leu	Met	Ser	Ser	Phe	Asn	Asp	Leu	Met	Gln	Arg	
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ctt	tgg	ata	gtc	gat	agc	gtt	gaa	cgt	ttg	ggg	ata	gct	aga	cat	ttc	494
Leu	Trp	Ile	Val	Asp	Ser	Val	Glu	Arg	Leu	Gly	Ile	Ala	Arg	His	Phe	
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aag	aac	gag	ata	aca	tca	gct	ctg	gat	tat	gtt	ttc	cgt	tac	tgg	gag	542
Lys	Asn	Glu	Ile	Thr	Ser	Ala	Leu	Asp	Tyr	Val	Phe	Arg	Tyr	Trp	Glu	
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Glu	Asn	Gly	Ile	Gly	Cys	Gly	Arg	Asp	Ser	Ile	Val	Thr	Asp	Leu	Asn	
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Ser	Thr	Ala	Leu	Gly	Phe	Arg	Thr	Leu	Arg	Leu	His	Gly	Tyr	Thr	Val	
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tct	cca	gag	gtt	tta	aaa	gct	ttt	caa	gat	caa	aat	gga	cag	ttt	gta	686
Ser	Pro	Glu	Val	Leu	Lys	Ala	Phe	Gln	Asp	Gln	Asn	Gly	Gln	Phe	Val	
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Cys	Ser	Pro	Gly	Gln	Thr	Glu	Gly	Glu	Ile	Arg	Ser	Val	Leu	Asn	Leu	
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Tyr	Arg	Ala	Ser	Leu	Ile	Ala	Phe	Pro	Gly	Glu	Lys	Val	Met	Glu	Glu	
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gct	gaa	atc	ttc	tcc	aca	aga	tat	ttg	aaa	gaa	gct	cta	caa	aag	att	830
Ala	Glu	Ile	Phe	Ser	Thr	Arg	Tyr	Leu	Lys	Glu	Ala	Leu	Gln	Lys	Ile	
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cca	gtc	tcc	gct	ctt	tca	caa	gag	ata	aag	ttt	gtt	atg	gaa	tat	ggc	878
Pro	Val	Ser	Ala	Leu	Ser	Gln	Glu	Ile	Lys	Phe	Val	Met	Glu	Tyr	Gly	
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ctt	gag	aaa	gac	acc	agt	gca	tgg	ctc	aat	aaa	aat	gct	ggg	aag	aag	974
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caa	aag	gaa	tta	caa	tat	ctt	ttg	aga	tgg	tgg	aaa	gag	tcg	gat	ttg	1070
Gln	Lys	Glu	Leu	Gln	Tyr	Leu	Leu	Arg	Trp	Trp	Lys	Glu	Ser	Asp	Leu	

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cct aaa ttg aca ttt gct cgg cat cgt cat gtg gaa ttc tac act ttg Pro Lys Leu Thr Phe Ala Arg His Arg His Val Glu Phe Tyr Thr Leu 335 340 345 350			1118
gcc tct tgt att gcc att gac cca aaa cat tct gca ttc aga cta ggc Ala Ser Cys Ile Ala Ile Asp Pro Lys His Ser Ala Phe Arg Leu Gly 355 360 365			1166
ttc gcc aaa atg tgt cat ctt gtc aca gtt ttg gac gat att tac gac Phe Ala Lys Met Cys His Leu Val Thr Val Leu Asp Asp Ile Tyr Asp 370 375 380			1214
act ttt gga acg att gac gag ctt gaa ctc ttc aca tct gca att aag Thr Phe Gly Thr Ile Asp Glu Leu Glu Leu Phe Thr Ser Ala Ile Lys 385 390 395			1262
aga tgg aat tca tca gag ata gaa cac ctt cca gaa tat atg aaa tgt Arg Trp Asn Ser Ser Glu Ile Glu His Leu Pro Glu Tyr Met Lys Cys 400 405 410			1310
gtg tac atg gtc gtg ttt gaa act gta aat gaa ctg aca cga gag gcg Val Tyr Met Val Val Phe Glu Thr Val Asn Glu Leu Thr Arg Glu Ala 415 420 425 430			1358
gag aag act caa ggg aga aac act ctc aac tat gtt cga aag gct tgg Glu Lys Thr Gln Gly Arg Asn Thr Leu Asn Tyr Val Arg Lys Ala Trp 435 440 445			1406
gag gct tat ttt gat tca tat atg gaa gaa gca aaa tgg atc tct aat Glu Ala Tyr Phe Asp Ser Tyr Met Glu Glu Ala Lys Trp Ile Ser Asn 450 455 460			1454
ggt tat ctg cca atg ttt gaa gag tac cat gag aat ggg aaa gtg agc Gly Tyr Leu Pro Met Phe Glu Glu Tyr His Glu Asn Gly Lys Val Ser 465 470 475			1502
tct gca tat cgc gta gca aca ttg caa ccc atc ctc act ttg aat gca Ser Ala Tyr Arg Val Ala Thr Leu Gln Pro Ile Leu Thr Leu Asn Ala 480 485 490			1550
tgg ctt cct gat tac atc ttg aag gga att gat ttt cca tcc agg ttc Trp Leu Pro Asp Tyr Ile Leu Lys Gly Ile Asp Phe Pro Ser Arg Phe 495 500 505 510			1598
aat gat ttg gca tcg tcc ttc ctt cgg cta cga ggt gac aca cgc tgc Asn Asp Leu Ala Ser Ser Phe Leu Arg Leu Arg Gly Asp Thr Arg Cys 515 520 525			1646
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tat atg aaa gac aat cct gga tca acc gaa gaa gat gcc ctc aat cat Tyr Met Lys Asp Asn Pro Gly Ser Thr Glu Glu Asp Ala Leu Asn His 545 550 555			1742
atc aat gcc atg gtc aat gac ata atc aaa gaa tta aat tgg gaa ctt Ile Asn Ala Met Val Asn Asp Ile Ile Lys Glu Leu Asn Trp Glu Leu 560 565 570			1790

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Leu Arg Ser Asn Asp Asn Ile Pro Met Leu Ala Lys Lys His Ala Phe
575 580 585 590

gac ata aca aga gct ctc cac cat ctc tac ata tat cga gat ggc ttt 1886
Asp Ile Thr Arg Ala Leu His His Leu Tyr Ile Tyr Arg Asp Gly Phe
595 600 605

agt gtt gcc aac aag gaa aca aaa aaa ttg gtt atg gaa aca ctc ctt 1934
Ser Val Ala Asn Lys Glu Thr Lys Lys Leu Val Met Glu Thr Leu Leu
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gaa tct atg ctt ttt taa ctataaccat atccataata ataagctcat 1982
Glu Ser Met Leu Phe
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Met Ser Ile Ser Leu Ala Thr Ala Ala Pro Asp Asp Gly Val Gln Arg 60
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Arg Ile Gly Asp Tyr His Ser Asn Ile Trp Asp Asp Asp Phe Ile Gln 80
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Ser Leu Ser Thr Pro Tyr Gly Glu Pro Ser Tyr Gln Glu Arg Ala Glu 95
85 90 95

Arg Leu Ile Val Glu Val Lys Lys Ile Phe Asn Ser Met Tyr Leu Asp 110
100 105 110

Asp Gly Arg Leu Met Ser Ser Phe Asn Asp Leu Met Gln Arg Leu Trp 125
115 120 125

Ile Val Asp Ser Val Glu Arg Leu Gly Ile Ala Arg His Phe Lys Asn 140
130 135 140

Glu Ile Thr Ser Ala Leu Asp Tyr Val Phe Arg Tyr Trp Glu Glu Asn 160
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Gly Ile Gly Cys Gly Arg Asp Ser Ile Val Thr Asp Leu Asn Ser Thr
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Ala Leu Gly Phe Arg Thr Leu Arg Leu His Gly Tyr Thr Val Ser Pro
180 185 190

Glu Val Leu Lys Ala Phe Gln Asp Gln Asn Gly Gln Phe Val Cys Ser
195 200 205

Pro Gly Gln Thr Glu Gly Glu Ile Arg Ser Val Leu Asn Leu Tyr Arg
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Ala Ser Leu Ile Ala Phe Pro Gly Glu Lys Val Met Glu Glu Ala Glu
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Ile Phe Ser Thr Arg Tyr Leu Lys Glu Ala Leu Gln Lys Ile Pro Val
245 250 255

Ser Ala Leu Ser Gln Glu Ile Lys Phe Val Met Glu Tyr Gly Trp His
260 265 270

Thr Asn Leu Pro Arg Leu Glu Ala Arg Asn Tyr Ile Asp Thr Leu Glu
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Lys Asp Thr Ser Ala Trp Leu Asn Lys Asn Ala Gly Lys Lys Leu Leu
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Glu Leu Ala Lys Leu Glu Phe Asn Ile Phe Asn Ser Leu Gln Gln Lys
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Leu Thr Phe Ala Arg His Arg His Val Glu Phe Tyr Thr Leu Ala Ser
340 345 350

Cys Ile Ala Ile Asp Pro Lys His Ser Ala Phe Arg Leu Gly Phe Ala
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Lys Met Cys His Leu Val Thr Val Leu Asp Asp Ile Tyr Asp Thr Phe
370 375 380

Gly Thr Ile Asp Glu Leu Glu Leu Phe Thr Ser Ala Ile Lys Arg Trp
385 390 395 400

Asn Ser Ser Glu Ile Glu His Leu Pro Glu Tyr Met Lys Cys Val Tyr
405 410 415

Met Val Val Phe Glu Thr Val Asn Glu Leu Thr Arg Glu Ala Glu Lys
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Tyr Arg Val Ala Thr Leu Gln Pro Ile Leu Thr Leu Asn Ala Trp Leu
485 490 495

Pro Asp Tyr Ile Leu Lys Gly Ile Asp Phe Pro Ser Arg Phe Asn Asp
500 505 510

Leu Ala Ser Ser Phe Leu Arg Leu Arg Gly Asp Thr Arg Cys Tyr Lys
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Ala Met Val Asn Asp Ile Ile Lys Glu Leu Asn Trp Glu Leu Leu Arg
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Thr Arg Ala Leu His His Leu Tyr Ile Tyr Arg Asp Gly Phe Ser Val
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Met Leu Phe
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<223> Clone AG3.18 encoding pinene synthase

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His Lys Ser Leu Ile Ser Ser Thr His Glu Leu Lys Ala Leu Ser Arg
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aca att cca gct cta gga atg agt agg cga ggg aaa tct atc act cct 146
Thr Ile Pro Ala Leu Gly Met Ser Arg Arg Gly Lys Ser Ile Thr Pro
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tcc atc agc atg agc tct acc acc gtt gta acc gat gat ggt gta cga 194
Ser Ile Ser Met Ser Ser Thr Thr Val Val Thr Asp Asp Gly Val Arg
50 55 60

aga cgc atg ggc gat ttc cat tcc aac ctc tgg gac gat gat gtc ata 242
Arg Arg Met Gly Asp Phe His Ser Asn Leu Trp Asp Asp Asp Val Ile
65 70 75

cag tct tta cca acg gct tat gag gaa aaa tcg tac ctg gag cgt gct Gln Ser Leu Pro Thr Ala Tyr Glu Glu Lys Ser Tyr Leu Glu Arg Ala 80	85	90	95	290
gag aaa ctg atc ggg gaa gta aag aac atg ttc aat tcg atg tca tta Glu Lys Leu Ile Gly Glu Val Lys Asn Met Phe Asn Ser Met Ser Leu 100	105	110		338
gaa gat gga gag tta atg agt ccg ctc aat gat ctc att caa cgc ctt Glu Asp Gly Glu Leu Met Ser Pro Leu Asn Asp Leu Ile Gln Arg Leu 115	120	125		386
tgg att gtc gac agc ctt gaa cgt ttg ggg atc cat aga cat ttc aaa Trp Ile Val Asp Ser Leu Glu Arg Leu Gly Ile His Arg His Phe Lys 130	135	140		434
gat gag ata aaa tcg gcg ctt gat tat gtt tac agt tat tgg ggc gaa Asp Glu Ile Lys Ser Ala Leu Asp Tyr Val Tyr Ser Tyr Trp Gly Glu 145	150	155		482
aat ggc atc gga tgc ggg agg gag agt gtt act gat ctg aac tca Asn Gly Ile Gly Cys Gly Arg Glu Ser Val Val Thr Asp Leu Asn Ser 160	165	170	175	530
act gcg ttg ggg ctt cga acc cta cga cta cac gga tac ccg gtg tct Thr Ala Leu Gly Leu Arg Thr Leu Arg Leu His Gly Tyr Pro Val Ser 180	185	190		578
tca gat gtt ttc aaa gct ttc aaa ggc caa aat ggg cag ttt tcc tgc Ser Asp Val Phe Lys Ala Phe Lys Gly Gln Asn Gly Gln Phe Ser Cys 195	200	205		626
tct gaa aat att cag aca gat gaa gag atc aga ggc gtt ctg aat tta Ser Glu Asn Ile Gln Thr Asp Glu Glu Ile Arg Gly Val Leu Asn Leu 210	215	220		674
ttc cgg gcc tcc ctc att gcc ttt cca ggg gag aaa att atg gat gag Phe Arg Ala Ser Leu Ile Ala Phe Pro Gly Glu Lys Ile Met Asp Glu 225	230	235		722
gct gaa atc ttc tct acc aaa tat tta aaa gaa gcc ctg caa aag att Ala Glu Ile Phe Ser Thr Lys Tyr Leu Lys Glu Ala Leu Gln Lys Ile 240	245	250	255	770
ccg gtc tcc agt ctt tcg cga gag atc ggg gac gtt ttg gaa tat ggt Pro Val Ser Ser Leu Ser Arg Glu Ile Gly Asp Val Leu Glu Tyr Gly 260	265	270		818
tgg cac aca tat ttg ccg cga ttg gaa gca agg aat tac atc caa gtc Trp His Thr Tyr Leu Pro Arg Leu Glu Ala Arg Asn Tyr Ile Gln Val 275	280	285		866
ttt gga cag gac act gag aac acg aag tca tat gtg aag agc aaa aaa Phe Gly Gln Asp Thr Glu Asn Thr Lys Ser Tyr Val Lys Ser Lys Lys 290	295	300		914
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aag agg gag tta gaa agt ctg gtc aga tgg tgg aaa gaa tcg ggt ttt Lys Arg Glu Leu Glu Ser Leu Val Arg Trp Trp Lys Glu Ser Gly Phe 320 325 330 335	1010
cct gag atg acc ttc tgc cga cat cgt cac gtg gaa tac tac act ttg Pro Glu Met Thr Phe Cys Arg His Arg His Val Glu Tyr Tyr Thr Leu 340 345 350	1058
gct tcc tgc att gcg ttc gag cct caa cat tct gga ttc aga ctc ggc Ala Ser Cys Ile Ala Phe Glu Pro Gln His Ser Gly Phe Arg Leu Gly 355 360 365	1106
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acc ttc ggc aca gta gac gag ctg gaa ctc ttc aca gcg aca atg aag Thr Phe Gly Thr Val Asp Glu Leu Glu Leu Phe Thr Ala Thr Met Lys 385 390 395	1202
aga tgg gat ccg tcc tcg ata gat tgc ctt cca gaa tat atg aaa gga Arg Trp Asp Pro Ser Ser Ile Asp Cys Leu Pro Glu Tyr Met Lys Gly 400 405 410 415	1250
gtg tac ata gcg gtt tac gac acc gta aat gaa atg gct cga gag gca Val Tyr Ile Ala Val Tyr Asp Thr Val Asn Glu Met Ala Arg Glu Ala 420 425 430	1298
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tac aag gcg gac agg gct cgt gga gaa gaa gct tcc tct ata tca tgt Tyr Lys Ala Asp Arg Ala Arg Gly Glu Glu Ala Ser Ser Ile Ser Cys 530 535 540	1634
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atc aac gcc atg atc agt gac gta atc aaa gga tta aat tgg gaa ctt	1730

Ile Asn Ala Met Ile Ser Asp Val Ile Lys Gly Leu Asn Trp Glu Leu
560 565 570 575

ctc aaa cca gac atc aat gtt ccc atc tcg gcg aag aaa cat gct ttt 1778
Leu Lys Pro Asp Ile Asn Val Pro Ile Ser Ala Lys Lys His Ala Phe
580 585 590

gac atc gcc aga gct ttc cat tac ggc tac aaa tac cga gac ggc tac 1826
Asp Ile Ala Arg Ala Phe His Tyr Gly Tyr Lys Tyr Arg Asp Gly Tyr
595 600 605

agc gtt gcc aac gtt gaa acg aag agt ttg gtc acg aga acc ctc ctt 1874
Ser Val Ala Asn Val Glu Thr Lys Ser Leu Val Thr Arg Thr Leu Leu
610 615 620

gaa tct gtg cct ttg tag caacagctca aatctatgcc ctatgctatg 1922
Glu Ser Val Pro Leu
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taataaagtt gtaatttaaa aaaaaaaaaaaa aaaaaaa 2018

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35 40 45

Ile Ser Met Ser Ser Thr Thr Val Val Thr Asp Asp Gly Val Arg Arg
50 55 60

Arg Met Gly Asp Phe His Ser Asn Leu Trp Asp Asp Asp Val Ile Gln
65 70 75 80

Ser Leu Pro Thr Ala Tyr Glu Glu Lys Ser Tyr Leu Glu Arg Ala Glu
85 90 95

Lys Leu Ile Gly Glu Val Lys Asn Met Phe Asn Ser Met Ser Leu Glu
100 105 110

Asp Gly Glu Leu Met Ser Pro Leu Asn Asp Leu Ile Gln Arg Leu Trp
115 120 125

Ile Val Asp Ser Leu Glu Arg Leu Gly Ile His Arg His Phe Lys Asp
130 135 140

Glu Ile Lys Ser Ala Leu Asp Tyr Val Tyr Ser Tyr Trp Gly Glu Asn
145 150 155 160

Gly Ile Gly Cys Gly Arg Glu Ser Val Val Thr Asp Leu Asn Ser Thr

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Asp Val Phe Lys Ala Phe Lys Gly Gln Asn	Gly Gln Phe Ser Cys Ser	
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Glu Asn Ile Gln Thr Asp Glu Glu Ile Arg	Gly Val Leu Asn Leu Phe	
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Arg Ala Ser Leu Ile Ala Phe Pro Gly Glu	Lys Ile Met Asp Glu Ala	
225	230	240
Glu Ile Phe Ser Thr Lys Tyr Leu Lys Glu	Ala Leu Gln Lys Ile Pro	
245	250	255
Val Ser Ser Leu Ser Arg Glu Ile Gly Asp	Val Leu Glu Tyr Gly Trp	
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His Thr Tyr Leu Pro Arg Leu Glu Ala Arg	Asn Tyr Ile Gln Val Phe	
275	280	285
Gly Gln Asp Thr Glu Asn Thr Lys Ser Tyr	Val Lys Ser Lys Lys Leu	
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Leu Glu Leu Ala Lys Leu Glu Phe Asn Ile	Phe Gln Ser Leu Gln Lys	
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Arg Glu Leu Glu Ser Leu Val Arg Trp Trp	Lys Glu Ser Gly Phe Pro	
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Glu Met Thr Phe Cys Arg His Arg His Val	Glu Tyr Tyr Thr Leu Ala	
340	345	350
Ser Cys Ile Ala Phe Glu Pro Gln His Ser	Gly Phe Arg Leu Gly Phe	
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Ala Lys Thr Cys His Leu Ile Thr Val Leu	Asp Asp Met Tyr Asp Thr	
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Phe Gly Thr Val Asp Glu Leu Glu Leu Phe	Thr Ala Thr Met Lys Arg	
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Ala Tyr Ile Asp Ser Tyr Met Gln Glu Ala	Arg Trp Ile Ala Thr Gly	
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Tyr Leu Pro Ser Phe Asp Glu Tyr Tyr Glu	Asn Gly Lys Val Ser Cys	
465	470	475
Gly His Arg Ile Ser Ala Leu Gln Pro Ile	Leu Thr Met Asp Ile Pro	
485	490	495

Phe Pro Asp His Ile Leu Lys Glu Val Asp Phe Pro Ser Lys Leu Asn
500 505 510

Asp Leu Ala Cys Ala Ile Leu Arg Leu Arg Gly Asp Thr Arg Cys Tyr
515 520 525

Lys Ala Asp Arg Ala Arg Gly Glu Glu Ala Ser Ser Ile Ser Cys Tyr
530 535 540

Met Lys Asp Asn Pro Gly Val Ser Glu Glu Asp Ala Leu Asp His Ile
545 550 555 560

Asn Ala Met Ile Ser Asp Val Ile Lys Gly Leu Asn Trp Glu Leu Leu
565 570 575

Lys Pro Asp Ile Asn Val Pro Ile Ser Ala Lys Lys His Ala Phe Asp
580 585 590

Ile Ala Arg Ala Phe His Tyr Gly Tyr Lys Tyr Arg Asp Gly Tyr Ser
595 600 605

Val Ala Asn Val Glu Thr Lys Ser Leu Val Thr Arg Thr Leu Leu Glu
610 615 620

Ser Val Pro Leu
625

<210> 5

<211> 2089

<212> DNA

<213> Abies grandis

<220>

<221> CDS

<222> (73)..(1986)

<223> Clone AG10 encoding limonene synthase

<400> 5

tgcgtttaa tcggttaaa gaagctacca tagtcggtt taaagaagct accatagtt 60

aggcaggaat cc atg gct ctc ctt tct atc gta tct ttg cag gtt ccc aaa 111
Met Ala Leu Leu Ser Ile Val Ser Leu Gln Val Pro Lys

1 5 10

tcc tgc ggg ctg aaa tcg ttg atc agt tcc agc aat gtg cag aag gct 159
Ser Cys Gly Leu Lys Ser Leu Ile Ser Ser Asn Val Gln Lys Ala
15 20 25

ctc tgt atc tct aca gca gtc cca aca ctc aga atg cgt agg cga cag 207
Leu Cys Ile Ser Thr Ala Val Pro Thr Leu Arg Met Arg Arg Arg Gln
30 35 40 45

aaa gct ctg gtc atc aac atg aaa ttg acc act gta tcc cat cgt gat 255
Lys Ala Leu Val Ile Asn Met Lys Leu Thr Thr Val Ser His Arg Asp
50 55 60

gat aat ggt ggt gta ctg caa aga cgc ata gcc gat cat cat ccc 303
Asp Asn Gly Gly Val Leu Gln Arg Arg Ile Ala Asp His His Pro
65 70 75

aac ctg tgg gaa gat gat ttc ata caa tca ttg tcc tca cct tat ggg Asn Leu Trp Glu Asp Asp Phe Ile Gln Ser Leu Ser Ser Pro Tyr Gly 80 85 90	351
gga tct tcg tac agt gaa cgt gct gag aca gtc gtt gag gaa gta aaa Gly Ser Ser Tyr Ser Glu Arg Ala Glu Thr Val Val Glu Glu Val Lys 95 100 105	399
gag atg ttc aat tca ata cca aat aat aga gaa tta ttt ggt tcc caa Glu Met Phe Asn Ser Ile Pro Asn Asn Arg Glu Leu Phe Gly Ser Gln 110 115 120 125	447
aat gat ctc ctt aca cgc ctt tgg atg gtg gat agc att gaa cgt ctg Asn Asp Leu Leu Thr Arg Leu Trp Met Val Asp Ser Ile Glu Arg Leu 130 135 140	495
ggg ata gat aga cat ttc caa aat gag ata aga gta gcc ctc gat tat Gly Ile Asp Arg His Phe Gln Asn Glu Ile Arg Val Ala Leu Asp Tyr 145 150 155	543
gtt tac agt tat tgg aag gaa aag gaa ggc att ggg tgt ggc aga gat Val Tyr Ser Tyr Trp Lys Glu Lys Glu Gly Ile Gly Cys Gly Arg Asp 160 165 170	591
tct act ttt cct gat ctc aac tcg act gcc ttg gcg ctt cga act ctt Ser Thr Phe Pro Asp Leu Asn Ser Thr Ala Leu Ala Leu Arg Thr Leu 175 180 185	639
cga ctg cac gga tac aat gtg tct tca gat gtg ctg gaa tac ttc aaa Arg Leu His Gly Tyr Asn Val Ser Ser Asp Val Leu Glu Tyr Phe Lys 190 195 200 205	687
gat gaa aag ggg cat ttt gcc tgc cct gca atc cta acc gag gga cag Asp Glu Lys Gly His Phe Ala Cys Pro Ala Ile Leu Thr Glu Gly Gln 210 215 220	735
atc act aga agt gtt cta aat tta tat cgg gct tcc ctg gtc gcc ttt Ile Thr Arg Ser Val Leu Asn Leu Tyr Arg Ala Ser Leu Val Ala Phe 225 230 235	783
ccc ggg gag aaa gtt atg gaa gag gct gaa atc ttc tcg gca tct tat Pro Gly Glu Lys Val Met Glu Glu Ala Glu Ile Phe Ser Ala Ser Tyr 240 245 250	831
ttg aaa aaa gtc tta caa aag att ccg gtc tcc aat ctt tca gga gag Leu Lys Lys Val Leu Gln Lys Ile Pro Val Ser Asn Leu Ser Gly Glu 255 260 265	879
ata gaa tat gtt ttg gaa tat ggt tgg cac acg aat ttg ccg aga ttg Ile Glu Tyr Val Leu Glu Tyr Gly Trp His Thr Asn Leu Pro Arg Leu 270 275 280 285	927
gaa gca aga aat tat atc gag gtc tac gag cag agc ggc tat gaa agc Glu Ala Arg Asn Tyr Ile Glu Val Tyr Glu Gln Ser Gly Tyr Glu Ser 290 295 300	975
tta aac gag atg cca tat atg aac atg aag aag ctt tta caa ctt gca Leu Asn Glu Met Pro Tyr Met Asn Met Lys Lys Leu Leu Gln Leu Ala 305 310 315	1023

aaa ttg gag ttc aat atc ttt cac tct ttg caa cta aga gag tta caa			1071
Lys Leu Glu Phe Asn Ile Phe His Ser Leu Gln Leu Arg Glu Leu Gln			
320	325	330	
tct atc tcc aga tgg tgg aaa gaa tca ggt tcg tct caa ctg act ttt			1119
Ser Ile Ser Arg Trp Trp Lys Glu Ser Gly Ser Ser Gln Leu Thr Phe			
335	340	345	
aca cgg cat cgt cac gtg gaa tac tac act atg gca tct tgc att tct			1167
Thr Arg His Arg His Val Glu Tyr Tyr Thr Met Ala Ser Cys Ile Ser			
350	355	360	365
atg ttg cca aaa cat tca gct ttc aga atg gag ttt gtc aaa gtg tgt			1215
Met Leu Pro Lys His Ser Ala Phe Arg Met Glu Phe Val Lys Val Cys			
370	375	380	
cat ctt gta aca gtt ctc gat gat ata tat gac act ttt gga aca atg			1263
His Leu Val Thr Val Leu Asp Asp Ile Tyr Asp Thr Phe Gly Thr Met			
385	390	395	
aac gaa ctccaa ctt ttt acg gat gca att aag aga tgg gat ttg tca			1311
Asn Glu Leu Gln Leu Phe Thr Asp Ala Ile Lys Arg Trp Asp Leu Ser			
400	405	410	
acg aca agg tgg ctt cca gaa tat atg aaa gga gtg tac atg gac ttg			1359
Thr Thr Arg Trp Leu Pro Glu Tyr Met Lys Gly Val Tyr Met Asp Leu			
415	420	425	
tat caa tgc att aat gaa atg gtg gaa gag gct gag aag act caa ggc			1407
Tyr Gln Cys Ile Asn Glu Met Val Glu Glu Ala Glu Lys Thr Gln Gly			
430	435	440	445
cga gat atg ctc aac tat att caa aat gct tgg gaa gcc cta ttt gat			1455
Arg Asp Met Leu Asn Tyr Ile Gln Asn Ala Trp Glu Ala Leu Phe Asp			
450	455	460	
acc ttt atg caa gaa gca aag tgg atc tcc agc agt tat ctc cca acg			1503
Thr Phe Met Gln Glu Ala Lys Trp Ile Ser Ser Tyr Leu Pro Thr			
465	470	475	
ttt gag gag tac ttg aag aat gca aaa gtt agt tct ggt tct cgc ata			1551
Phe Glu Glu Tyr Leu Lys Asn Ala Lys Val Ser Ser Gly Ser Arg Ile			
480	485	490	
gcc aca tta caa ccc att ctc act ttg gat gta cca ctt cct gat tac			1599
Ala Thr Leu Gln Pro Ile Leu Thr Leu Asp Val Pro Leu Pro Asp Tyr			
495	500	505	
ata ctg caa gaa att gat tat cca tcc aga ttc aat gag tta gct tcg			1647
Ile Leu Gln Glu Ile Asp Tyr Pro Ser Arg Phe Asn Glu Leu Ala Ser			
510	515	520	525
tcc atc ctt cga cta cga ggt gac acg cgc tgc tac aag gcg gat agg			1695
Ser Ile Leu Arg Leu Arg Gly Asp Thr Arg Cys Tyr Lys Ala Asp Arg			
530	535	540	
gcc cgt gga gaa gaa gct tca gct ata tcg tgt tat atg aaa gac cat			1743
Ala Arg Gly Glu Glu Ala Ser Ala Ile Ser Cys Tyr Met Lys Asp His			
545	550	555	
cct gga tca ata gag gaa gat gct ctc aat cat atc aac gcc atg atc			1791

Pro Gly Ser Ile Glu Glu Asp Ala Leu Asn His Ile Asn Ala Met Ile
560 565 570

agt gat gca atc aga gaa tta aat tgg gag ctt ctc aga ccg gat agc 1839
Ser Asp Ala Ile Arg Glu Leu Asn Trp Glu Leu Leu Arg Pro Asp Ser
575 580 585

aaa agt ccc atc tct tcc aag aaa cat gct ttt gac atc acc aga gct 1887
Lys Ser Pro Ile Ser Ser Lys Lys His Ala Phe Asp Ile Thr Arg Ala
590 595 600 605

ttc cat cat gtc tac aaa tat cga gat ggt tac act gtt tcc aac aac 1935
Phe His His Val Tyr Lys Tyr Arg Asp Gly Tyr Thr Val Ser Asn Asn
610 615 620

gaa aca aag aat ttg gtg atg aaa acc gtt ctt gaa cct ctc gct ttg 1983
Glu Thr Lys Asn Leu Val Met Lys Thr Val Leu Glu Pro Leu Ala Leu
625 630 635

taa aaacatatacg aatgcattaa aatgtggaa gtctataatc tagactattc 2036

tctatcttcc ataatgtaga tctggatgtg tattgaactc taaaaaaaaaaa aaa 2089

<210> 6
<211> 637
<212> PRT
<213> Abies grandis

<400> 6
Met Ala Leu Leu Ser Ile Val Ser Leu Gln Val Pro Lys Ser Cys Gly
1 5 10 15

Leu Lys Ser Leu Ile Ser Ser Asn Val Gln Lys Ala Leu Cys Ile
20 25 30

Ser Thr Ala Val Pro Thr Leu Arg Met Arg Arg Arg Gln Lys Ala Leu
35 40 45

Val Ile Asn Met Lys Leu Thr Thr Val Ser His Arg Asp Asp Asn Gly
50 55 60

Gly Gly Val Leu Gln Arg Arg Ile Ala Asp His His Pro Asn Leu Trp
65 70 75 80

Glu Asp Asp Phe Ile Gln Ser Leu Ser Ser Pro Tyr Gly Gly Ser Ser
85 90 95

Tyr Ser Glu Arg Ala Glu Thr Val Val Glu Glu Val Lys Glu Met Phe
100 105 110

Asn Ser Ile Pro Asn Asn Arg Glu Leu Phe Gly Ser Gln Asn Asp Leu
115 120 125

Leu Thr Arg Leu Trp Met Val Asp Ser Ile Glu Arg Leu Gly Ile Asp
130 135 140

Arg His Phe Gln Asn Glu Ile Arg Val Ala Leu Asp Tyr Val Tyr Ser
145 150 155 160

Tyr Trp Lys Glu Lys Glu Gly Ile Gly Cys Gly Arg Asp Ser Thr Phe
165 170 175

Pro Asp Leu Asn Ser Thr Ala Leu Ala Leu Arg Thr Leu Arg Leu His
180 185 190

Gly Tyr Asn Val Ser Ser Asp Val Leu Glu Tyr Phe Lys Asp Glu Lys
195 200 205

Gly His Phe Ala Cys Pro Ala Ile Leu Thr Glu Gly Gln Ile Thr Arg
210 215 220

Ser Val Leu Asn Leu Tyr Arg Ala Ser Leu Val Ala Phe Pro Gly Glu
225 230 235 240

Lys Val Met Glu Glu Ala Glu Ile Phe Ser Ala Ser Tyr Leu Lys Lys
245 250 255

Val Leu Gln Lys Ile Pro Val Ser Asn Leu Ser Gly Glu Ile Glu Tyr
260 265 270

Val Leu Glu Tyr Gly Trp His Thr Asn Leu Pro Arg Leu Glu Ala Arg
275 280 285

Asn Tyr Ile Glu Val Tyr Glu Gln Ser Gly Tyr Glu Ser Leu Asn Glu
290 295 300

Met Pro Tyr Met Asn Met Lys Lys Leu Leu Gln Leu Ala Lys Leu Glu
305 310 315 320

Phe Asn Ile Phe His Ser Leu Gln Leu Arg Glu Leu Gln Ser Ile Ser
325 330 335

Arg Trp Trp Lys Glu Ser Gly Ser Ser Gln Leu Thr Phe Thr Arg His
340 345 350

Arg His Val Glu Tyr Tyr Thr Met Ala Ser Cys Ile Ser Met Leu Pro
355 360 365

Lys His Ser Ala Phe Arg Met Glu Phe Val Lys Val Cys His Leu Val
370 375 380

Thr Val Leu Asp Asp Ile Tyr Asp Thr Phe Gly Thr Met Asn Glu Leu
385 390 395 400

Gln Leu Phe Thr Asp Ala Ile Lys Arg Trp Asp Leu Ser Thr Thr Arg
405 410 415

Trp Leu Pro Glu Tyr Met Lys Gly Val Tyr Met Asp Leu Tyr Gln Cys
420 425 430

Ile Asn Glu Met Val Glu Glu Ala Glu Lys Thr Gln Gly Arg Asp Met
435 440 445

Leu Asn Tyr Ile Gln Asn Ala Trp Glu Ala Leu Phe Asp Thr Phe Met
450 455 460

Gln Glu Ala Lys Trp Ile Ser Ser Ser Tyr Leu Pro Thr Phe Glu Glu
465 470 475 480

Tyr Leu Lys Asn Ala Lys Val Ser Ser Gly Ser Arg Ile Ala Thr Leu

485	490	495
Gln Pro Ile Leu Thr Leu Asp Val Pro Leu Pro Asp Tyr Ile Leu Gln		
500	505	510
Glu Ile Asp Tyr Pro Ser Arg Phe Asn Glu Leu Ala Ser Ser Ile Leu		
515	520	525
Arg Leu Arg Gly Asp Thr Arg Cys Tyr Lys Ala Asp Arg Ala Arg Gly		
530	535	540
Glu Glu Ala Ser Ala Ile Ser Cys Tyr Met Lys Asp His Pro Gly Ser		
545	550	555
Ile Glu Glu Asp Ala Leu Asn His Ile Asn Ala Met Ile Ser Asp Ala		
565	570	575
Ile Arg Glu Leu Asn Trp Glu Leu Leu Arg Pro Asp Ser Lys Ser Pro		
580	585	590
Ile Ser Ser Lys Lys His Ala Phe Asp Ile Thr Arg Ala Phe His His		
595	600	605
Val Tyr Lys Tyr Arg Asp Gly Tyr Thr Val Ser Asn Asn Glu Thr Lys		
610	615	620
Asn Leu Val Met Lys Thr Val Leu Glu Pro Leu Ala Leu		
625	630	635

<210> 7
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Degenerate oligonucleotide PCR primer A wherein the letter "n" indicates an inosine residue

<220>
<221> misc_feature
<222> (1)..(25)
<223> Degenerate oligonucleotide Primer A wherein n represents inosine

<400> 7
arraygarra nggnrartay aarga 25

<210> 8
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: degenerate oligonucleotide PCR primer B wherein the letter "n" represents an inosine residue

<220>

<221> misc_feature
<222> (1)..(20)
<223> oligonucleotide PCR primer B wherein the letter n
represents an inosine residue

<400> 8
atgytnccary tntaygargc 20

<210> 9
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: degenerate
oligonucleotide PCR primer C wherein the letter
"n" represents an inosine residue

<220>
<221> misc_feature
<222> (1)..(24)
<223> PCR primer C wherein the letter n represents
inosine

<400> 9
ctnkynrang gnctratrtta ckyt 24

<210> 10
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: degenerate
oligonucleotide PCR primer D wherein the letter
"n" represents an inosine residue

<220>
<221> misc_feature
<222> (1)..(23)
<223> PCR primer D wherein the letter n represents
inosine

<400> 10
gaygaynnnt wygaygcnya ygg 23

<210> 11
<211> 108
<212> DNA
<213> Artificial Sequence

<400> 11
gatgatgggt ttgatgcgca cggaacccta gatgaattga agctattcac tgaggctgtg 60
agaagatggg acctctcctt tacagacaac ttccccgatt acatgaaa 108

<210> 12

<211> 104

<212> DNA

<213> Abies grandis

<400> 12

gacgacgggt atgatgcga tggaacgatt gacgagctt aactcttcac atctgcaatt 60

aagagatgga attcatcaga gatacacgc ttcccccact atat

104

<210> 13

<211> 105

<212> DNA

<213> Abies grandis

<220>

<221> misc_feature

<222> (89)

<223> nucleotide may be a or c or g or t

<400> 13

gatgatgggt atgatgcgt a cggAACGTTT gaagaaatca aaatcatgac agagggagt 60

agacgatggg atcttcgtt gaccgcttnc cccgactata tgaaa

105

<210> 14

<211> 117

<212> DNA

<213> Abies grandis

<220>

<221> misc_feature

<222> (93)

<223> nucleotide may be a or c or g or t

<400> 14

gacgatgggt atgatgcga tggaacctt gaccaactca aaatcttac agagggagt 60

agacgatggg atcttcgtt ggttagaccac ttnccccac tacatgcaat ctagacc 117

<210> 15

<211> 2424

<212> DNA

<213> Abies grandis

<220>

<221> CDS

<222> (2)..(2350)

<223> Clone AG1.28

<400> 15

g ggt tat gat ctt gtg cat tct ctt aaa tca cct tat att gat tct agt 49

Gly Tyr Asp Leu Val His Ser Leu Lys Ser Pro Tyr Ile Asp Ser Ser

1 5 10 15

tac aga gaa cgc gcg gag gtc ctt gtt agc gag att aaa gtg atg ctt 97

Tyr Arg Glu Arg Ala Glu Val Leu Val Ser Glu Ile Lys Val Met Leu

20 25 30

aat cca gct att aca gga gat gga gaa tca atg att act cca tct gct			145
Asn Pro Ala Ile Thr Gly Asp Gly Glu Ser Met Ile Thr Pro Ser Ala			
35	40	45	
tat gac aca gca tgg gta gcg agg gtg ccc gcc att gat ggc tct gct			193
Tyr Asp Thr Ala Trp Val Ala Arg Val Pro Ala Ile Asp Gly Ser Ala			
50	55	60	
cgc ccg caa ttt ccc caa aca gtt gac tgg att ttg aaa aac cag tta			241
Arg Pro Gln Phe Pro Gln Thr Val Asp Trp Ile Leu Lys Asn Gln Leu			
65	70	75	80
aaa gat ggt tca tgg gga att cag tcc cac ttt ctg ctg tcc gac cgt			289
Lys Asp Gly Ser Trp Gly Ile Gln Ser His Phe Leu Leu Ser Asp Arg			
85	90	95	
ctt ctt gcc act ctt tct tgt gtt ctt gtg ctc ctt aaa tgg aac gtt			337
Leu Leu Ala Thr Leu Ser Cys Val Leu Val Leu Leu Lys Trp Asn Val			
100	105	110	
ggg gat ctg caa gta gag cag gga att gaa ttc ata aag agc aat ctg			385
Gly Asp Leu Gln Val Glu Gln Gly Ile Glu Phe Ile Lys Ser Asn Leu			
115	120	125	
gaa cta gta aag gat gaa acc gat caa gat agc ttg gta aca gac ttt			433
Glu Leu Val Lys Asp Glu Thr Asp Gln Asp Ser Leu Val Thr Asp Phe			
130	135	140	
gag atc ata ttt cct tct ctg tta aga gaa gct caa tct ctg cgc ctc			481
Glu Ile Ile Phe Pro Ser Leu Leu Arg Glu Ala Gln Ser Leu Arg Leu			
145	150	155	160
gga ctt ccc tac gac ctg cct tat ata cat ctg ttg cag act aaa cgg			529
Gly Leu Pro Tyr Asp Leu Pro Tyr Ile His Leu Leu Gln Thr Lys Arg			
165	170	175	
cag gaa aga tta gca aaa ctt tca agg gag gaa att tat gcg gtt ccg			577
Gln Glu Arg Leu Ala Lys Leu Ser Arg Glu Glu Ile Tyr Ala Val Pro			
180	185	190	
tcg cca ttg ttg tat tct tta gag gga ata caa gat ata gtt gaa tgg			625
Ser Pro Leu Leu Tyr Ser Leu Glu Gly Ile Gln Asp Ile Val Glu Trp			
195	200	205	
gaa cga ata atg gaa gtt caa agt cag gat ggg tct ttc tta agc tca			673
Glu Arg Ile Met Glu Val Gln Ser Gln Asp Gly Ser Phe Leu Ser Ser			
210	215	220	
cct gct tct act gcc tgc gtt ttc atg cac aca gga gac gcg aaa tgc			721
Pro Ala Ser Thr Ala Cys Val Phe Met His Thr Gly Asp Ala Lys Cys			
225	230	235	240
ctt gaa ttc ttg aac agt gtg atg atc aag ttt gga aat ttt gtt ccc			769
Leu Glu Phe Leu Asn Ser Val Met Ile Lys Phe Gly Asn Phe Val Pro			
245	250	255	
tgc ctg tat cct gtg gat ctg ctg gaa cgc ctg ttg atc gta gat aat			817
Cys Leu Tyr Pro Val Asp Leu Leu Glu Arg Leu Leu Ile Val Asp Asn			
260	265	270	
att gta cgc ctt gga atc tat aga cac ttt gaa aag gaa atc aag gaa			865

Ile Val Arg Leu Gly Ile Tyr Arg His Phe Glu Lys Glu Ile Lys Glu			
275	280	285	
gct ctt gat tat gtt tac agg cat tgg aac gaa aga gga att ggg tgg			913
Ala Leu Asp Tyr Val Tyr Arg His Trp Asn Glu Arg Gly Ile Gly Trp			
290	295	300	
ggc aga cta aat ccc ata gca gat ctt gag acc act gct ttg gga ttt			961
Gly Arg Leu Asn Pro Ile Ala Asp Leu Glu Thr Thr Ala Leu Gly Phe			
305	310	315	320
cga ttg ctt cgg ctg cat agg tac aat gta tct cca gcc att ttt gac			1009
Arg Leu Leu Arg Leu His Arg Tyr Asn Val Ser Pro Ala Ile Phe Asp			
325	330	335	
aac ttc aaa gat gcc aat ggg aaa ttc att tgc tcg acc ggt caa ttc			1057
Asn Phe Lys Asp Ala Asn Gly Lys Phe Ile Cys Ser Thr Gly Gln Phe			
340	345	350	
aac aaa gat gta gca agc atg ctg aat ctt tat aga gct tcc cag ctc			1105
Asn Lys Asp Val Ala Ser Met Leu Asn Leu Tyr Arg Ala Ser Gln Leu			
355	360	365	
gca ttt ccc gga gaa aac att ctt gat gaa gct aaa agc ttc gct act			1153
Ala Phe Pro Gly Glu Asn Ile Leu Asp Glu Ala Lys Ser Phe Ala Thr			
370	375	380	
aaa tat ttg aga gaa gct ctt gag aaa agt gag act tcc agt gca tgg			1201
Lys Tyr Leu Arg Glu Ala Leu Glu Lys Ser Glu Thr Ser Ser Ala Trp			
385	390	395	400
aac aac aaa caa aac ctg agc caa gag atc aaa tac gcg ctg aag act			1249
Asn Asn Lys Gln Asn Leu Ser Gln Glu Ile Lys Tyr Ala Leu Lys Thr			
405	410	415	
tct tgg cat gcc agt gtt ccg aga gtg gaa gca aag aga tac tgt caa			1297
Ser Trp His Ala Ser Val Pro Arg Val Glu Ala Lys Arg Tyr Cys Gln			
420	425	430	
gtg tat cgc cca gat tat gca cgc ata gca aaa tgc gtt tac aag cta			1345
Val Tyr Arg Pro Asp Tyr Ala Arg Ile Ala Lys Cys Val Tyr Lys Leu			
435	440	445	
ccc tac gtg aac aat gaa aag ttt tta gag ctg gga aaa tta gat ttc			1393
Pro Tyr Val Asn Asn Glu Lys Phe Leu Glu Leu Gly Lys Leu Asp Phe			
450	455	460	
aac att atc cag tcc atc cac caa gaa gaa atg aag aat gtt acc agc			1441
Asn Ile Ile Gln Ser Ile His Gln Glu Glu Met Lys Asn Val Thr Ser			
465	470	475	480
tgg ttt aga gat tcg ggg ttg cca cta ttc acc ttc gct cggt gag agg			1489
Trp Phe Arg Asp Ser Gly Leu Pro Leu Phe Thr Phe Ala Arg Glu Arg			
485	490	495	
ccg ctg gaa ttc tac ttc tta gta gcg gcg ggg acc tat gaa ccc cag			1537
Pro Leu Glu Phe Tyr Phe Leu Val Ala Ala Gly Thr Tyr Glu Pro Gln			
500	505	510	
tat gcc aaa tgc agg ttc ctc ttt aca aaa gtg gca tgc ttg cag act			1585
Tyr Ala Lys Cys Arg Phe Leu Phe Thr Lys Val Ala Cys Leu Gln Thr			

515	520	525	
gtt ctg gac gat atg tat gac act tat gga acc cta gat gaa ttg aag Val Leu Asp Asp Met Tyr Asp Thr Tyr Gly Thr Leu Asp Glu Leu Lys 530	535	540	1633
cta ttc act gag gct gtg aga aga tgg gac ctc tcc ttt aca gaa aac Leu Phe Thr Glu Ala Val Arg Arg Trp Asp Leu Ser Phe Thr Glu Asn 545	550	555	1681
ctt cca gac tat atg aaa cta tgt tac caa atc tat tat gac ata gtt Leu Pro Asp Tyr Met Lys Leu Cys Tyr Gln Ile Tyr Tyr Asp Ile Val 565	570	575	1729
cac gag gtg gct tgg gag gca gag aag gaa cag ggg cgt gaa ttg gtc His Glu Val Ala Trp Glu Ala Glu Lys Glu Gln Gly Arg Glu Leu Val 580	585	590	1777
agc ttt ttc aga aag gga tgg gag gat tat ctt ctg ggt tat tat gaa Ser Phe Phe Arg Lys Gly Trp Glu Asp Tyr Leu Leu Gly Tyr Tyr Glu 595	600	605	1825
gaa gct gaa tgg tta gct gct gag tat gtg cct acc ttg gac gag tac Glu Ala Glu Trp Leu Ala Ala Glu Tyr Val Pro Thr Leu Asp Glu Tyr 610	615	620	1873
ata aag aat gga atc aca tct atc ggc caa cgt ata ctt ctg ttg agt Ile Lys Asn Gly Ile Thr Ser Ile Gly Gln Arg Ile Leu Leu Leu Ser 625	630	635	1921
gga gtg ttg ata atg gat ggg caa ctc ctt tcg caa gag gca tta gag Gly Val Leu Ile Met Asp Gly Gln Leu Leu Ser Gln Glu Ala Leu Glu 645	650	655	1969
aaa gta gat tat cca gga aga cgt gtt ctc aca gag ctg aat agc ctc Lys Val Asp Tyr Pro Gly Arg Arg Val Leu Thr Glu Leu Asn Ser Leu 660	665	670	2017
att tcc cgc ctg gcg gat gac acg aag aca tat aaa gct gag aag gct Ile Ser Arg Leu Ala Asp Asp Thr Lys Thr Tyr Lys Ala Glu Lys Ala 675	680	685	2065
cgt gga gaa ttg gcg tcc agc att gaa tgt tac atg aaa gac cat cct Arg Gly Glu Leu Ala Ser Ser Ile Glu Cys Tyr Met Lys Asp His Pro 690	695	700	2113
gaa tgt aca gag gaa gag gct ctc gat cac atc tat agc att ctg gag Glu Cys Thr Glu Glu Ala Leu Asp His Ile Tyr Ser Ile Leu Glu 705	710	715	2161
ccg gcg gtg aag gaa ctg aca aga gag ttt ctg aag ccc gac gac gtc Pro Ala Val Lys Glu Leu Thr Arg Glu Phe Leu Lys Pro Asp Asp Val 725	730	735	2209
cca ttc gcc tgc aag aag atg ctt ttc gag gag aca aga gtg acg atg Pro Phe Ala Cys Lys Lys Met Leu Phe Glu Glu Thr Arg Val Thr Met 740	745	750	2257
gtg ata ttc aag gat gga gat gga ttc ggt gtt tcc aaa tta gaa gtc Val Ile Phe Lys Asp Gly Asp Gly Phe Gly Val Ser Lys Leu Glu Val 755	760	765	2305

aaa gat cat atc aaa gag tgt ctc att gaa ccg ctg cca ctg taa 2350
Lys Asp His Ile Lys Glu Cys Leu Ile Glu Pro Leu Pro Leu
770 775 780

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Asn Pro Ala Ile Thr Gly Asp Gly Glu Ser Met Ile Thr Pro Ser Ala
35 40 45

Tyr Asp Thr Ala Trp Val Ala Arg Val Pro Ala Ile Asp Gly Ser Ala
50 55 60

Arg Pro Gln Phe Pro Gln Thr Val Asp Trp Ile Leu Lys Asn Gln Leu
65 70 75 80

Lys Asp Gly Ser Trp Gly Ile Gln Ser His Phe Leu Leu Ser Asp Arg
85 90 95

Leu Leu Ala Thr Leu Ser Cys Val Leu Val Leu Lys Trp Asn Val
100 105 110

Gly Asp Leu Gln Val Glu Gln Gly Ile Glu Phe Ile Lys Ser Asn Leu
115 120 125

Glu Leu Val Lys Asp Glu Thr Asp Gln Asp Ser Leu Val Thr Asp Phe
130 135 140

Glu Ile Ile Phe Pro Ser Leu Leu Arg Glu Ala Gln Ser Leu Arg Leu
145 150 155 160

Gly Leu Pro Tyr Asp Leu Pro Tyr Ile His Leu Leu Gln Thr Lys Arg
165 170 175

Gln Glu Arg Leu Ala Lys Leu Ser Arg Glu Glu Ile Tyr Ala Val Pro
180 185 190

Ser Pro Leu Leu Tyr Ser Leu Glu Gly Ile Gln Asp Ile Val Glu Trp
195 200 205

Glu Arg Ile Met Glu Val Gln Ser Gln Asp Gly Ser Phe Leu Ser Ser
210 215 220

Pro Ala Ser Thr Ala Cys Val Phe Met His Thr Gly Asp Ala Lys Cys
225 230 235 240

Leu Glu Phe Leu Asn Ser Val Met Ile Lys Phe Gly Asn Phe Val Pro
245 250 255

Cys Leu Tyr Pro Val Asp Leu Leu Glu Arg Leu Leu Ile Val Asp Asn
260 265 270

Ile Val Arg Leu Gly Ile Tyr Arg His Phe Glu Lys Glu Ile Lys Glu
275 280 285

Ala Leu Asp Tyr Val Tyr Arg His Trp Asn Glu Arg Gly Ile Gly Trp
290 295 300

Gly Arg Leu Asn Pro Ile Ala Asp Leu Glu Thr Thr Ala Leu Gly Phe
305 310 315 320

Arg Leu Leu Arg Leu His Arg Tyr Asn Val Ser Pro Ala Ile Phe Asp
325 330 335

Asn Phe Lys Asp Ala Asn Gly Lys Phe Ile Cys Ser Thr Gly Gln Phe
340 345 350

Asn Lys Asp Val Ala Ser Met Leu Asn Leu Tyr Arg Ala Ser Gln Leu
355 360 365

Ala Phe Pro Gly Glu Asn Ile Leu Asp Glu Ala Lys Ser Phe Ala Thr
370 375 380

Lys Tyr Leu Arg Glu Ala Leu Glu Lys Ser Glu Thr Ser Ser Ala Trp
385 390 395 400

Asn Asn Lys Gln Asn Leu Ser Gln Glu Ile Lys Tyr Ala Leu Lys Thr
405 410 415

Ser Trp His Ala Ser Val Pro Arg Val Glu Ala Lys Arg Tyr Cys Gln
420 425 430

Val Tyr Arg Pro Asp Tyr Ala Arg Ile Ala Lys Cys Val Tyr Lys Leu
435 440 445

Pro Tyr Val Asn Asn Glu Lys Phe Leu Glu Leu Gly Lys Leu Asp Phe
450 455 460

Asn Ile Ile Gln Ser Ile His Gln Glu Glu Met Lys Asn Val Thr Ser
465 470 475 480

Trp Phe Arg Asp Ser Gly Leu Pro Leu Phe Thr Phe Ala Arg Glu Arg
485 490 495

Pro Leu Glu Phe Tyr Phe Leu Val Ala Ala Gly Thr Tyr Glu Pro Gln
500 505 510

Tyr Ala Lys Cys Arg Phe Leu Phe Thr Lys Val Ala Cys Leu Gln Thr
515 520 525

Val Leu Asp Asp Met Tyr Asp Thr Tyr Gly Thr Leu Asp Glu Leu Lys
530 535 540

Leu Phe Thr Glu Ala Val Arg Arg Trp Asp Leu Ser Phe Thr Glu Asn
545 550 555 560

Leu Pro Asp Tyr Met Lys Leu Cys Tyr Gln Ile Tyr Tyr Asp Ile Val

565	570	575
His Glu Val Ala Trp Glu Ala Glu Lys Glu Gln Gly Arg Glu Leu Val		
580	585	590
Ser Phe Phe Arg Lys Gly Trp Glu Asp Tyr Leu Leu Gly Tyr Tyr Glu		
595	600	605
Glu Ala Glu Trp Leu Ala Ala Glu Tyr Val Pro Thr Leu Asp Glu Tyr		
610	615	620
Ile Lys Asn Gly Ile Thr Ser Ile Gly Gln Arg Ile Leu Leu Leu Ser		
625	630	635
Gly Val Leu Ile Met Asp Gly Gln Leu Leu Ser Gln Glu Ala Leu Glu		
645	650	655
Lys Val Asp Tyr Pro Gly Arg Arg Val Leu Thr Glu Leu Asn Ser Leu		
660	665	670
Ile Ser Arg Leu Ala Asp Asp Thr Lys Thr Tyr Lys Ala Glu Lys Ala		
675	680	685
Arg Gly Glu Leu Ala Ser Ser Ile Glu Cys Tyr Met Lys Asp His Pro		
690	695	700
Glu Cys Thr Glu Glu Glu Ala Leu Asp His Ile Tyr Ser Ile Leu Glu		
705	710	715
720		
Pro Ala Val Lys Glu Leu Thr Arg Glu Phe Leu Lys Pro Asp Asp Val		
725	730	735
Pro Phe Ala Cys Lys Lys Met Leu Phe Glu Glu Thr Arg Val Thr Met		
740	745	750
Val Ile Phe Lys Asp Gly Asp Gly Phe Gly Val Ser Lys Leu Glu Val		
755	760	765
Lys Asp His Ile Lys Glu Cys Leu Ile Glu Pro Leu Pro Leu		
770	775	780

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 Ser Glu Ser Ser Ile Pro Arg Arg Thr Gly Asn His His Gly Asn
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gtg tgg gac gat gac ctc ata cac tct ctc aac tcg ccc tat ggg gca 95
Val Trp Asp Asp Asp Leu Ile His Ser Leu Asn Ser Pro Tyr Gly Ala
 20 25 30

cct gca tat tat gag ctc ctt caa aag ctt att gag gag atc aag cat			143
Pro Ala Tyr Tyr Glu Leu Leu Gln Lys Leu Ile Glu Glu Ile Lys His			
35	40	45	
tta ctt ttg act gaa atg gaa atg gat gat ggc gat cat gat tta atc			191
Leu Leu Leu Thr Glu Met Glu Met Asp Asp Gly Asp His Asp Leu Ile			
50	55	60	
aaa cgt ctt cag atc gtt gac act ttg gaa tgc ctg gga atc gat aga			239
Lys Arg Leu Gln Ile Val Asp Thr Leu Glu Cys Leu Gly Ile Asp Arg			
65	70	75	
cat ttt gaa cac gaa ata caa aca gct gct tta gat tac gtt tac aga			287
His Phe Glu His Glu Ile Gln Thr Ala Ala Leu Asp Tyr Val Tyr Arg			
80	85	90	95
tgg tgg aac gaa aaa ggt atc ggg gag gga tca aga gat tcc ttc agc			335
Trp Trp Asn Glu Lys Gly Ile Gly Glu Gly Ser Arg Asp Ser Phe Ser			
100	105	110	
aaa gat ctc aac gct aca gct tta gga ttt cgc gct ctc cga ctg cat			383
Lys Asp Leu Asn Ala Thr Ala Leu Gly Phe Arg Ala Leu Arg Leu His			
115	120	125	
cga tat aac gta tcg tca ggt gtg ttg aag aat ttc aag gat gaa aac			431
Arg Tyr Asn Val Ser Ser Gly Val Leu Lys Asn Phe Lys Asp Glu Asn			
130	135	140	
ggg aag ttc ttc tgc aac ttt act ggt gaa gaa gga aga gga gat aaa			479
Gly Lys Phe Phe Cys Asn Phe Thr Gly Glu Glu Gly Arg Gly Asp Lys			
145	150	155	
caa gtg aga agc atg ttg tcg tta ctt cga gct tca gag att tcg ttt			527
Gln Val Arg Ser Met Leu Ser Leu Leu Arg Ala Ser Glu Ile Ser Phe			
160	165	170	175
ccc gga gaa aaa gtg atg gaa gag gcc aag gca ttc aca aga gaa tat			575
Pro Gly Glu Lys Val Met Glu Glu Ala Lys Ala Phe Thr Arg Glu Tyr			
180	185	190	
cta aac caa gtt tta gct gga cac ggg gat gtg act gac gtg gat caa			623
Leu Asn Gln Val Leu Ala Gly His Gly Asp Val Thr Asp Val Asp Gln			
195	200	205	
agc ctt ttg gag aga ggt gaa gta cgc att gga gtt tcc atg gct tgc			671
Ser Leu Leu Glu Arg Gly Glu Val Arg Ile Gly Val Ser Met Ala Cys			
210	215	220	
agt gtg ccg aga tgg gag gca agg agc ttt ctc gaa ata tat gga cac			719
Ser Val Pro Arg Trp Glu Ala Arg Ser Phe Leu Glu Ile Tyr Gly His			
225	230	235	
aac cat tcg tgg ctc aag tcg aat atc aac caa aaa atg ttg aag tta			767
Asn His Ser Trp Leu Lys Ser Asn Ile Asn Gln Lys Met Leu Lys Leu			
240	245	250	255
gcc aaa ttg gac ttc aat att ctg caa tgc aaa cat cac aag gag ata			815
Ala Lys Leu Asp Phe Asn Ile Leu Gln Cys Lys His His Lys Glu Ile			
260	265	270	
cag ttt att aca agg tgg tgg aga gac tcg ggt ata tcg cag ctg aat			863

Gln	Phe	Ile	Thr	Arg	Trp	Trp	Arg	Asp	Ser	Gly	Ile	Ser	Gln	Leu	Asn			
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ttc	tat	cga	aag	cga	cac	gtg	gaa	tat	tat	tct	tgg	gtt	gtt	atg	tgc	911		
Phe	Tyr	Arg	Lys	Arg	His	Val	Glu	Tyr	Tyr	Ser	Trp	Val	Val	Met	Cys			
290																300		
att	ttt	gag	cca	gag	ttc	tct	gaa	agt	aga	att	gcc	ttc	gcc	aaa	act	959		
Ile	Phe	Glu	Pro	Glu	Phe	Ser	Glu	Ser	Arg	Ile	Ala	Phe	Ala	Lys	Thr			
305																315		
gct	atc	cta	tgt	act	gtt	cta	gat	gac	ctc	tat	gat	acg	cac	gca	acg	1007		
Ala	Ile	Leu	Cys	Thr	Val	Leu	Asp	Asp	Leu	Tyr	Asp	Thr	His	Ala	Thr			
320																335		
ttg	cat	gaa	atc	aaa	atc	atg	aca	gag	gga	gtg	aga	cga	tgg	gat	ctt	1055		
Leu	His	Glu	Ile	Lys	Ile	Met	Thr	Glu	Gly	Val	Arg	Arg	Trp	Asp	Leu			
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tcg	ttg	aca	gat	gac	ctc	cca	gac	tac	att	aaa	att	gca	ttc	cag	ttc	1103		
Ser	Leu	Thr	Asp	Asp	Leu	Pro	Asp	Tyr	Ile	Lys	Ile	Ala	Phe	Gln	Phe			
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Phe	Phe	Asn	Thr	Val	Asn	Glu	Leu	Ile	Val	Glu	Ile	Val	Lys	Arg	Gln			
370																380		
ggg	cg	gat	atg	aca	acc	ata	gtt	aaa	gat	tgc	tgg	aag	cga	tac	att	1199		
Gly	Arg	Asp	Met	Thr	Thr	Ile	Val	Lys	Asp	Cys	Trp	Lys	Arg	Tyr	Ile			
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gag	tct	tat	ctg	caa	gaa	g	g	g	tgg	ata	gca	act	g	g	cat	att	ccc	1247
Glu	Ser	Tyr	Leu	Gln	Glu	Ala	Glu	Trp	Ile	Ala	Thr	Gly	His	Ile	Pro			
400																410	415	
act	ttt	aac	gaa	tac	ata	aag	aa	cc	gg	at	g	ct	gg	at	tg	1295		
Thr	Phe	Asn	Glu	Tyr	Ile	Lys	Asn	Gly	Met	Ala	Ser	Ser	Gly	Met	Cys			
420																430		
att	gta	aat	ttg	aat	cca	ctt	ctc	ttg	ttg	ggt	aaa	ctt	ctc	ccc	gac	1343		
Ile	Val	Asn	Leu	Asn	Pro	Leu	Leu	Leu	Leu	Gly	Lys	Leu	Leu	Pro	Asp			
435																445		
aac	att	ctg	gag	caa	ata	cat	tct	cca	tcc	aag	atc	ctg	gac	ctc	tta	1391		
Asn	Ile	Leu	Glu	Gln	Ile	His	Ser	Pro	Ser	Lys	Ile	Leu	Asp	Leu	Leu			
450																455	460	
gaa	ttg	acg	ggc	aga	atc	gcc	gat	gac	tta	aaa	gat	ttc	gag	gac	gag	1439		
Glu	Leu	Thr	Gly	Arg	Ile	Ala	Asp	Asp	Leu	Lys	Asp	Phe	Glu	Asp	Glu			
465																470	475	
aag	gaa	cgc	ggg	gag	atg	g	c	t	t	c	g	t	t	at	g	aaa	gaa	1487
Lys	Glu	Arg	Gly	Glu	Met	Ala	Ser	Ser	Leu	Gln	Cys	Tyr	Met	Lys	Glu			
480																485	490	495
aat	cct	gaa	tct	aca	gtg	gaa	aat	g	c	t	a	c	a	aa	gg	atc	1535	
Asn	Pro	Glu	Ser	Thr	Val	Glu	Asn	Ala	Leu	Asn	His	Ile	Lys	Gly	Ile			
500																505	510	
ctt	aat	cgt	tcc	ctt	gag	gaa	ttt	aat	tgg	gag	ttt	at	g	a	g	at	1583	
Leu	Asn	Arg	Ser	Leu	Glu	Glu	Phe	Asn	Trp	Glu	Phe	Met	Lys	Gln	Asp			

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agt gtc cca atg tgt tgc aag aaa ttc act ttc aat ata ggt cga gga Ser Val Pro Met Cys Cys Lys Lys Phe Thr Phe Asn Ile Gly Arg Gly 530	535	540	1631
ctt caa ttc atc tac aaa tac aga gac ggc tta tac att tct gac aag Leu Gln Phe Ile Tyr Lys Tyr Arg Asp Gly Leu Tyr Ile Ser Asp Lys 545	550	555	1679
gaa gta aag gac cag ata ttc aaa att cta gtc cac caa gtt cca atg Glu Val Lys Asp Gln Ile Phe Lys Ile Leu Val His Gln Val Pro Met 560	565	570	1727
gag gaa tag tgatggtctt ggtttagtt gtctattatg gtatattgca Glu Glu			1776
ttgacattta tgcttaaagg tgtttcttaa acgttttaggg cgaccgtta aataagttgg caataattaa tatttagaga ctgttgaa gtgttttaggg cataaaaattt cctatggcct atggcaagct acaaatttggaa attgttgtgt ttataatatt tttatttat taaaaaaaaa aaaaaaaaaa a			1836
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Leu Leu Thr Glu Met Glu Met Asp Asp Gly Asp His Asp Leu Ile Lys 50 55 60			
Arg Leu Gln Ile Val Asp Thr Leu Glu Cys Leu Gly Ile Asp Arg His 65 70 75 80			
Phe Glu His Glu Ile Gln Thr Ala Ala Leu Asp Tyr Val Tyr Arg Trp 85 90 95			
Trp Asn Glu Lys Gly Ile Gly Glu Gly Ser Arg Asp Ser Phe Ser Lys 100 105 110			
Asp Leu Asn Ala Thr Ala Leu Gly Phe Arg Ala Leu Arg Leu His Arg 115 120 125			
Tyr Asn Val Ser Ser Gly Val Leu Lys Asn Phe Lys Asp Glu Asn Gly 130 135 140			
Lys Phe Phe Cys Asn Phe Thr Gly Glu Glu Gly Arg Gly Asp Lys Gln 145 150 155 160			

Val Arg Ser Met Leu Ser Leu Leu Arg Ala Ser Glu Ile Ser Phe Pro
165 170 175

Gly Glu Lys Val Met Glu Glu Ala Lys Ala Phe Thr Arg Glu Tyr Leu
180 185 190

Asn Gln Val Leu Ala Gly His Gly Asp Val Thr Asp Val Asp Gln Ser
195 200 205

Leu Leu Glu Arg Gly Glu Val Arg Ile Gly Val Ser Met Ala Cys Ser
210 215 220

Val Pro Arg Trp Glu Ala Arg Ser Phe Leu Glu Ile Tyr Gly His Asn
225 230 235 240

His Ser Trp Leu Lys Ser Asn Ile Asn Gln Lys Met Leu Lys Leu Ala
245 250 255

Lys Leu Asp Phe Asn Ile Leu Gln Cys Lys His His Lys Glu Ile Gln
260 265 270

Phe Ile Thr Arg Trp Trp Arg Asp Ser Gly Ile Ser Gln Leu Asn Phe
275 280 285

Tyr Arg Lys Arg His Val Glu Tyr Tyr Ser Trp Val Val Met Cys Ile
290 295 300

Phe Glu Pro Glu Phe Ser Glu Ser Arg Ile Ala Phe Ala Lys Thr Ala
305 310 315 320

Ile Leu Cys Thr Val Leu Asp Asp Leu Tyr Asp Thr His Ala Thr Leu
325 330 335

His Glu Ile Lys Ile Met Thr Glu Gly Val Arg Arg Trp Asp Leu Ser
340 345 350

Leu Thr Asp Asp Leu Pro Asp Tyr Ile Lys Ile Ala Phe Gln Phe Phe
355 360 365

Phe Asn Thr Val Asn Glu Leu Ile Val Glu Ile Val Lys Arg Gln Gly
370 375 380

Arg Asp Met Thr Thr Ile Val Lys Asp Cys Trp Lys Arg Tyr Ile Glu
385 390 395 400

Ser Tyr Leu Gln Glu Ala Glu Trp Ile Ala Thr Gly His Ile Pro Thr
405 410 415

Phe Asn Glu Tyr Ile Lys Asn Gly Met Ala Ser Ser Gly Met Cys Ile
420 425 430

Val Asn Leu Asn Pro Leu Leu Leu Gly Lys Leu Leu Pro Asp Asn
435 440 445

Ile Leu Glu Gln Ile His Ser Pro Ser Lys Ile Leu Asp Leu Leu Glu
450 455 460

Leu Thr Gly Arg Ile Ala Asp Asp Leu Lys Asp Phe Glu Asp Glu Lys
465 470 475 480

Glu Arg Gly Glu Met Ala Ser Ser Leu Gln Cys Tyr Met Lys Glu Asn
485 490 495

Pro Glu Ser Thr Val Glu Asn Ala Leu Asn His Ile Lys Gly Ile Leu
500 505 510

Asn Arg Ser Leu Glu Glu Phe Asn Trp Glu Phe Met Lys Gln Asp Ser
515 520 525

Val Pro Met Cys Cys Lys Lys Phe Thr Phe Asn Ile Gly Arg Gly Leu
530 535 540

Gln Phe Ile Tyr Lys Tyr Arg Asp Gly Leu Tyr Ile Ser Asp Lys Glu
545 550 555 560

Val Lys Asp Gln Ile Phe Lys Ile Leu Val His Gln Val Pro Met Glu
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Lys Val Leu Ala Gly Arg Glu Ala Thr His Val Asp Glu Ser Leu Leu
20 25 30

gga gag gtg aag tac gca ttg gag ttt cca tgg cat tgc agt gtg cag 143
Gly Glu Val Lys Tyr Ala Leu Glu Phe Pro Trp His Cys Ser Val Gln
35 40 45

aga tgg gag gca agg agc ttt atc gaa ata ttt gga caa att gat tca 191
Arg Trp Glu Ala Arg Ser Phe Ile Glu Ile Phe Gly Gln Ile Asp Ser
50 55 60

gag ctt aag tcg aat ttg agc aaa aaa atg tta gag ttg gcg aaa ttg 239
Glu Leu Lys Ser Asn Leu Ser Lys Lys Met Leu Glu Leu Ala Lys Leu
65 70 75

gac ttc aat att ctg caa tgc aca cat cag aaa gaa ctg cag att atc 287
Asp Phe Asn Ile Leu Gln Cys Thr His Gln Lys Glu Leu Gln Ile Ile
80 85 90 95

tca agg tgg ttc gca gac tca agt ata gca tcc ctg aat ttc tat cgg 335
Ser Arg Trp Phe Ala Asp Ser Ser Ile Ala Ser Leu Asn Phe Tyr Arg
100 105 110

aaa tgt tac gtc gaa ttt tac ttt tgg atg gct gca gcc atc tcc gag 383

Lys	Cys	Tyr	Val	Glu	Phe	Tyr	Phe	Trp	Met	Ala	Ala	Ala	Ile	Ser	Glu	
			115					120					125			
ccg	gag	ttt	tct	gga	agc	aga	gtt	gcc	ttc	aca	aaa	att	gct	ata	ctg	431
Pro	Glu	Phe	Ser	Gly	Ser	Arg	Val	Ala	Phe	Thr	Lys	Ile	Ala	Ile	Leu	
			130					135				140				
atg	aca	atg	cta	gat	gac	ctg	tac	gat	act	cac	gga	acc	ttg	gac	caa	479
Met	Thr	Met	Leu	Asp	Asp	Leu	Tyr	Asp	Thr	His	Gly	Thr	Leu	Asp	Gln	
			145					150			155					
ctc	aaa	atc	ttt	aca	gag	gga	gtg	aga	cga	tgg	gat	gtt	tcg	ttg	gta	527
Leu	Lys	Ile	Phe	Thr	Glu	Gly	Val	Arg	Arg	Trp	Asp	Val	Ser	Leu	Val	
			160				165			170			175			
gag	ggc	ctc	cca	gac	ttc	atg	aaa	att	gca	ttc	gag	ttc	tgg	tta	aag	575
Glu	Gly	Leu	Pro	Asp	Phe	Met	Lys	Ile	Ala	Phe	Glu	Phe	Trp	Leu	Lys	
			180					185			190					
aca	tct	aat	gaa	ttg	att	gct	gaa	gct	gtt	aaa	gcg	caa	ggg	caa	gat	623
Thr	Ser	Asn	Glu	Leu	Ile	Ala	Glu	Ala	Val	Lys	Ala	Gln	Gly	Gln	Asp	
			195					200			205					
atg	gcg	gcc	tac	ata	aga	aaa	aat	gca	tgg	gag	cga	tac	ctt	gaa	gct	671
Met	Ala	Ala	Tyr	Ile	Arg	Lys	Asn	Ala	Trp	Glu	Arg	Tyr	Leu	Glu	Ala	
			210				215			220						
tat	ctg	caa	gat	gcg	gaa	tgg	ata	gcc	act	gga	cat	gtc	ccc	acc	ttt	719
Tyr	Leu	Gln	Asp	Ala	Glu	Trp	Ile	Ala	Thr	Gly	His	Val	Pro	Thr	Phe	
			225				230			235						
gat	gag	tac	ttg	aat	aat	ggc	aca	cca	aac	act	ggg	atg	tgt	gta	ttg	767
Asp	Glu	Tyr	Leu	Asn	Asn	Gly	Thr	Pro	Asn	Thr	Gly	Met	Cys	Val	Leu	
			240				245			250			255			
aat	ttg	att	ccg	ctt	ctg	tta	atg	ggt	gaa	cat	tta	cca	atc	gac	att	815
Asn	Leu	Ile	Pro	Leu	Leu	Leu	Met	Gly	Glu	His	Leu	Pro	Ile	Asp	Ile	
			260					265			270					
ctg	gag	caa	ata	ttc	ttg	ccc	tcc	agg	ttc	cac	cat	ctc	att	gaa	ttg	863
Leu	Glu	Gln	Ile	Phe	Leu	Pro	Ser	Arg	Phe	His	His	Leu	Ile	Glu	Leu	
			275				280			285						
gct	tcc	agg	ctc	gtc	gat	gac	gcg	aga	gat	ttc	cag	gcg	gag	aag	gat	911
Ala	Ser	Arg	Leu	Val	Asp	Asp	Ala	Arg	Asp	Phe	Gln	Ala	Glu	Lys	Asp	
			290				295			300						
cat	ggg	gat	tta	tcg	tgt	att	gag	tgt	tat	tta	aaa	gat	cat	cct	gag	959
His	Gly	Asp	Leu	Ser	Cys	Ile	Glu	Cys	Tyr	Leu	Lys	Asp	His	Pro	Glu	
			305				310			315						
tct	aca	gta	gaa	gat	gct	tta	aat	cat	gtt	aat	ggc	ctc	ctt	ggc	aat	1007
Ser	Thr	Val	Glu	Asp	Ala	Leu	Asn	His	Val	Asn	Gly	Leu	Leu	Gly	Asn	
			320				325			330			335			
tgc	ctt	ctg	gaa	atg	aat	tgg	aag	ttc	tta	aag	aag	cag	gac	agt	gtg	1055
Cys	Leu	Leu	Glu	Met	Asn	Trp	Lys	Phe	Leu	Lys	Lys	Gln	Asp	Ser	Val	
			340					345			350					
cca	ctc	tcg	tgt	aag	aag	tac	agc	ttc	cat	gta	ttg	gca	cga	agc	atc	1103
Pro	Leu	Ser	Cys	Lys	Lys	Tyr	Ser	Phe	His	Val	Leu	Ala	Arg	Ser	Ile	

355

360

365

caa ttc atg tac aat caa ggc gat ggc ttc tcc att tcg aac aaa gtg 1151
Gln Phe Met Tyr Asn Gln Gly Asp Gly Phe Ser Ile Ser Asn Lys Val
370 375 380

atc aag gat caa gtg cag aaa gtt ctt att gtc ccc gtg cct att tga 1199
Ile Lys Asp Gln Val Gln Lys Val Leu Ile Val Pro Val Pro Ile
385 390 395

tagtagatac tagatagtag attagtagct attagtattt atttcataatc aatatattact 1259

aatgctgatg atggtaaaag tccattcaga ccaatcttg gtttattgga cttaaataaa 1319

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<212> PRT

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Glu Val Lys Tyr Ala Leu Glu Phe Pro Trp His Cys Ser Val Gln Arg
35 40 45

Trp Glu Ala Arg Ser Phe Ile Glu Ile Phe Gly Gln Ile Asp Ser Glu
50 55 60

Leu Lys Ser Asn Leu Ser Lys Lys Met Leu Glu Leu Ala Lys Leu Asp
65 70 75 80

Phe Asn Ile Leu Gln Cys Thr His Gln Lys Glu Leu Gln Ile Ile Ser
85 90 95

Arg Trp Phe Ala Asp Ser Ser Ile Ala Ser Leu Asn Phe Tyr Arg Lys
100 105 110

Cys Tyr Val Glu Phe Tyr Phe Trp Met Ala Ala Ala Ile Ser Glu Pro
115 120 125

Glu Phe Ser Gly Ser Arg Val Ala Phe Thr Lys Ile Ala Ile Leu Met
130 135 140

Thr Met Leu Asp Asp Leu Tyr Asp Thr His Gly Thr Leu Asp Gln Leu
145 150 155 160

Lys Ile Phe Thr Glu Gly Val Arg Arg Trp Asp Val Ser Leu Val Glu
165 170 175

Gly Leu Pro Asp Phe Met Lys Ile Ala Phe Glu Phe Trp Leu Lys Thr
180 185 190

Ser Asn Glu Leu Ile Ala Glu Ala Val Lys Ala Gln Gly Gln Asp Met
195 200 205

Ala Ala Tyr Ile Arg Lys Asn Ala Trp Glu Arg Tyr Leu Glu Ala Tyr
210 215 220

Leu Gln Asp Ala Glu Trp Ile Ala Thr Gly His Val Pro Thr Phe Asp
225 230 235 240

Glu Tyr Leu Asn Asn Gly Thr Pro Asn Thr Gly Met Cys Val Leu Asn
245 250 255

Leu Ile Pro Leu Leu Met Gly Glu His Leu Pro Ile Asp Ile Leu
260 265 270

Glu Gln Ile Phe Leu Pro Ser Arg Phe His His Leu Ile Glu Leu Ala
275 280 285

Ser Arg Leu Val Asp Asp Ala Arg Asp Phe Gln Ala Glu Lys Asp His
290 295 300

Gly Asp Leu Ser Cys Ile Glu Cys Tyr Leu Lys Asp His Pro Glu Ser
305 310 315 320

Thr Val Glu Asp Ala Leu Asn His Val Asn Gly Leu Leu Gly Asn Cys
325 330 335

Leu Leu Glu Met Asn Trp Lys Phe Leu Lys Lys Gln Asp Ser Val Pro
340 345 350

Leu Ser Cys Lys Lys Tyr Ser Phe His Val Leu Ala Arg Ser Ile Gln
355 360 365

Phe Met Tyr Asn Gln Gly Asp Gly Phe Ser Ile Ser Asn Lys Val Ile
370 375 380

Lys Asp Gln Val Gln Lys Val Leu Ile Val Pro Val Pro Ile
385 390 395

<210> 21

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
oligonucleotide PCR primer E wherein the letter
"n" represents an inosine residue

<220>

<221> misc_feature

<222> (1)..(23)

<223> PCR primer E wherein the letter n represents
inosine

<400> 21

ggngaramrr tnatggarga rgc

23

<210> 22

<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: degenerate oligonucleotide primer F wherein the letter "n" represents an inosine residue

<220>
<221> misc_feature
<222> (1)..(24)
<223> PCR primer F wherein the letter n represents inosine

<400> 22
garytnccary tnhbnmgntg gtgg 24

<210> 23
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: degenerate oligonucleotide PCR primer G wherein the letter "n" represents an inosine residue

<220>
<221> misc_feature
<222> (1)..(21)
<223> PCR primer G wherein the letter n represents inosine

<400> 23
ccarttnarn ccyttnacrt c 21

<210> 24
<211> 533
<212> DNA
<213> Abies grandis

<400> 24
ggggaaaaaaa tgatggagga agctgaaatc ttctctacca aatatttaaa agaagccctg 60
caaaaaggattc cggtctccag tcttcgcga gagatcgaaa acgttttggaa atatggttgg 120
cacacatatt tgccgcgatt ggaagcaagg aattacatcc aagtctttgg acaggacact 180
gagaacacga agtcatatgt gaagagcaaa aaacttttag aactcgcaaa attggagttc 240
aacatcttcc aatccttact cgcataatccg cattgcaacc cattctgaca atggacatcc 300
ccttcctga tcataatcctc aaggaagttt acttcccattc aaagcttaac gacttggcat 360
gtgccatcct tcgattacga ggtgatacgc ggtgctacaa ggccggacagg gctcgtggag 420
aagaagcttc ctcttatatca tgtttatatga aagacaatcc tggagtatca gaggaagatg 480

ctctcgatca tatcaacgcc atgatcagtg acgaagtcaa aggcttcaat tgg 533

<210> 25
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: conserved amino acid motif on which the sequence of Primer D was based, wherein Xaa at position number 3 represents Thr or Ile, Xaa at position number 4 represents Ile or Tyr or Phe, Xaa at position number 6 represents Ala or Val and Xaa at position number 8 represents Ala or Gly

<220>
<221> SITE
<222> (1)..(8)
<223> conserved amino acid motif on which sequence of primer D was based

<400> 25
Asp Asp Xaa Xaa Asp Xaa Tyr Xaa
1 5

<210> 26
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: conserved amino acid motif on which the sequence of Primer E was based wherein Xaa at position 3 represents Lys or Thr, Xaa at position 4 represents Val or Ile, Xaa at position 6 represents Glu or Asp

<220>
<221> SITE
<222> (1)..(8)
<223> conserved amino acid sequence on which the sequence of primer E was based

<400> 26
Gly Glu Xaa Xaa Met Xaa Glu Ala
1 5

<210> 27
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: conserved amino acid sequence on which the sequence of primer F was based wherein Xaa at position 2 represents Phe or Tyr or Asp

Xaa at position 3 represents Ile or Leu, Xaa at position 4 represents Thr or Leu
or Arg

<220>
<221> SITE
<222> (1)..(7)
<223> conserved amino acid sequence on which the sequence of primer F was based

<400> 27
Gln Xaa Xaa Xaa Arg Trp Trp
1 5

<210> 28
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: conserved amino acid motif on which the sequence of primer G was based wherein Xaa at position 6 represents Phe or Leu

<220>
<221> SITE
<222> (1)..(8)
<223> conserved amino acid sequence on which the sequence of primer G was based

<400> 28
Asp Val Ile Lys Gly Xaa Asn Trp
1 5

<210> 29
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: T3 primer oligonucleotide sequence

<400> 29
aattaaccct cactaaaggg 20

<210> 30
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: T7 oligonucleotide primer sequence

<400> 30
gtaatacgac tcactatagg gc 22

<210> 31
<211> 2205
<212> DNA
<213> Abies grandis

<220>
<221> CDS
<222> (57)..(1943)
<223> Clone AG3.48

<400> 31
gttatcttga gtttcctcca tataggccaa cacatatcat atcaaaggga gcaaga atg 59
Met
1

gct ctg gtt tct atc tca ccg ttg gct tcg aaa tct tgc ctg cgc aag 107
Ala Leu Val Ser Ile Ser Pro Leu Ala Ser Lys Ser Cys Leu Arg Lys
5 10 15

tcg ttg atc agt tca att cat gaa cat aag cct ccc tat aga aca atc 155
Ser Leu Ile Ser Ser Ile His Glu His Lys Pro Pro Tyr Arg Thr Ile
20 25 30

cca aat ctt gga atg cgt agg cga ggg aaa tct gtc acg cct tcc atg 203
Pro Asn Leu Gly Met Arg Arg Gly Lys Ser Val Thr Pro Ser Met
35 40 45

agc atc agt ttg gcc acc gct gca cct gat gat ggt gta caa aga cgc 251
Ser Ile Ser Leu Ala Thr Ala Ala Pro Asp Asp Gly Val Gln Arg Arg
50 55 60 65

ata ggt gac tac cat tcc aat atc tgg gac gat gat ttc ata cag tct 299
Ile Gly Asp Tyr His Ser Asn Ile Trp Asp Asp Asp Phe Ile Gln Ser
70 75 80

cta tca acg cat tat ggg gaa ccc tct tac cag gaa cgt gct gag aga 347
Leu Ser Thr His Tyr Gly Glu Pro Ser Tyr Gln Glu Arg Ala Glu Arg
85 90 95

tta att gtg gag gta aag aag ata ttc aat tca atg tac ctg gat gat 395
Leu Ile Val Glu Val Lys Lys Ile Phe Asn Ser Met Tyr Leu Asp Asp
100 105 110

gga aga tta atg agt tcc ttt aat gat ctc atg caa cgc ctt tgg ata 443
Gly Arg Leu Met Ser Ser Phe Asn Asp Leu Met Gln Arg Leu Trp Ile
115 120 125

gtc gat agc gtt gaa cgt ttg ggg ata gct aga cat ttc aag aac gag 491
Val Asp Ser Val Glu Arg Leu Gly Ile Ala Arg His Phe Lys Asn Glu
130 135 140 145

ata aca tca gct ctg gat tat gtt ttc cgt tac tgg gag gaa aac ggc 539
Ile Thr Ser Ala Leu Asp Tyr Val Phe Arg Tyr Trp Glu Glu Asn Gly
150 155 160

att gga tgt ggg aga gac agt att gtt act gat ctc aac tca act gcg 587
Ile Gly Cys Gly Arg Asp Ser Ile Val Thr Asp Leu Asn Ser Thr Ala
165 170 175

ttg ggg ttt cga act ctt cga tta cac ggg tac act gta tct cca gag 635

Leu	Gly	Phe	Arg	Thr	Leu	Arg	Leu	His	Gly	Tyr	Thr	Val	Ser	Pro	Glu	
180					185							190				
gtt	tta	aaa	gct	ttt	caa	gat	caa	aat	gga	cag	ttt	gta	tgc	tcc	ccc	683
Val	Leu	Lys	Ala	Phe	Gln	Asp	Gln	Asn	Gly	Gln	Phe	Val	Cys	Ser	Pro	
195					200							205				
ggt	cag	aca	gag	ggt	gag	atc	aga	agc	gtt	ctt	aac	tta	tat	cgg	gct	731
Gly	Gln	Thr	Glu	Gly	Glu	Ile	Arg	Ser	Val	Leu	Asn	Leu	Tyr	Arg	Ala	
210					215							220			225	
tcc	ctc	att	gcc	ttc	cct	ggt	gag	aaa	gtt	atg	gaa	gaa	gct	gaa	atc	779
Ser	Leu	Ile	Ala	Phe	Pro	Gly	Glu	Lys	Val	Met	Glu	Glu	Ala	Glu	Ile	
					230					235			240			
ttc	tcc	aca	aga	tat	ttg	aaa	gaa	gct	cta	caa	aag	att	cca	gtc	tcc	827
Phe	Ser	Thr	Arg	Tyr	Leu	Lys	Glu	Ala	Leu	Gln	Lys	Ile	Pro	Val	Ser	
					245					250			255			
gct	ctt	tca	caa	gag	ata	aag	ttt	gtt	atg	gaa	tat	ggc	tgg	cac	aca	875
Ala	Leu	Ser	Gln	Glu	Ile	Lys	Phe	Val	Met	Glu	Tyr	Gly	Trp	His	Thr	
					260					265			270			
aat	ttg	cca	aga	ttg	gaa	gca	aga	aat	tac	ata	gac	aca	ctt	gag	aaa	923
Asn	Leu	Pro	Arg	Leu	Glu	Ala	Arg	Asn	Tyr	Ile	Asp	Thr	Leu	Glu	Lys	
					275					280			285			
gac	acc	agt	gca	tgg	ctc	aat	aaa	aat	gct	ggg	aag	aag	ctt	tta	gaa	971
Asp	Thr	Ser	Ala	Trp	Leu	Asn	Lys	Asn	Ala	Gly	Lys	Lys	Leu	Glu		
					290					295			300		305	
ctt	gca	aaa	ttg	gag	ttc	aat	ata	ttt	aac	tcc	tta	caa	caa	aag	gaa	1019
Leu	Ala	Lys	Leu	Glu	Phe	Asn	Ile	Phe	Asn	Ser	Leu	Gln	Gln	Lys	Glu	
					310					315			320			
tta	caa	tat	ctt	ttg	aga	tgg	tgg	aaa	gag	tcg	gat	ttg	cct	aaa	ttg	1067
Leu	Gln	Tyr	Leu	Leu	Arg	Trp	Trp	Lys	Glu	Ser	Asp	Leu	Pro	Lys	Leu	
					325					330			335			
aca	ttt	gct	cgg	cat	cgt	cat	gtg	gaa	ttc	tac	act	ttg	gcc	tct	tgt	1115
Thr	Phe	Ala	Arg	His	Arg	His	Val	Glu	Phe	Tyr	Thr	Leu	Ala	Ser	Cys	
					340					345			350			
att	gcc	att	gac	cca	aaa	cat	tct	gca	ttc	aga	cta	ggc	ttc	gcc	aaa	1163
Ile	Ala	Ile	Asp	Pro	Lys	His	Ser	Ala	Phe	Arg	Leu	Gly	Phe	Ala	Lys	
					355					360			365			
atg	tgt	cat	ctt	gtc	aca	gtt	ttg	gac	gat	att	tac	gac	act	ttt	gga	1211
Met	Cys	His	Leu	Val	Thr	Val	Leu	Asp	Asp	Ile	Tyr	Asp	Thr	Phe	Gly	
					370					375			380		385	
acg	att	gac	gag	ctt	gaa	ctc	ttc	aca	tct	gca	att	aag	aga	tgg	aat	1259
Thr	Ile	Asp	Glu	Leu	Glu	Ieu	Phe	Thr	Ser	Ala	Ile	Lys	Arg	Trp	Asn	
					390					395			400			
tca	tca	gag	ata	gaa	cac	ctt	cca	gaa	tat	atg	aaa	tgt	gtg	tac	atg	1307
Ser	Ser	Glu	Ile	Glu	His	Leu	Pro	Glu	Tyr	Met	Lys	Cys	Val	Tyr	Met	
					405					410			415			
gtc	gtg	ttt	gaa	act	gta	aat	gaa	ctg	aca	cga	gag	gcf	gag	aag	act	1355
Val	Val	Phe	Glu	Thr	Val	Asn	Glu	Leu	Thr	Arg	Glu	Ala	Glu	Lys	Thr	

420	425	430	
caa ggg aga aac act ctc aac tat gtt cga aag gct tgg gag gct tat Gln Gly Arg Asn Thr Leu Asn Tyr Val Arg Lys Ala Trp Glu Ala Tyr 435	440	445	1403
ttt gat tca tat atg gaa gaa gca aaa tgg atc tct aat ggt tat ctg Phe Asp Ser Tyr Met Glu Glu Ala Lys Trp Ile Ser Asn Gly Tyr Leu 450	455	460	1451
cca acg ttt gaa gag tac cat gag aat ggg aaa gtg agc tct gca tat Pro Thr Phe Glu Glu Tyr His Glu Asn Gly Lys Val Ser Ser Ala Tyr 470	475	480	1499
cgc gta gca aca ttg caa ccc atc ctc act ttg aat gca tgg ctt cct Arg Val Ala Thr Leu Gln Pro Ile Leu Thr Leu Asn Ala Trp Leu Pro 485	490	495	1547
gat tac atc ttg aag gga att gat ttt cca tcc agg ttc aat gat ttg Asp Tyr Ile Leu Lys Gly Ile Asp Phe Pro Ser Arg Phe Asn Asp Leu 500	505	510	1595
gca tcg tcc ttc ctt cg ^g cta cga ggt gac aca cgc tgc tac aag gcc Ala Ser Ser Phe Leu Arg Leu Arg Gly Asp Thr Arg Cys Tyr Lys Ala 515	520	525	1643
gat agg gat cgt ggt gaa gaa gct tcg tgt ata tca tgt tat atg aaa Asp Arg Asp Arg Gly Glu Glu Ala Ser Cys Ile Ser Cys Tyr Met Lys 530	535	540	1691
gac aat cct gga tca acc gaa gaa gat gcc ctc aat cat atc aat gcc Asp Asn Pro Gly Ser Thr Glu Glu Asp Ala Leu Asn His Ile Asn Ala 550	555	560	1739
atg gtc aat gac ata atc aaa gaa tta aat tgg gaa ctt cta aga tcc Met Val Asn Asp Ile Ile Lys Glu Leu Asn Trp Glu Leu Leu Arg Ser 565	570	575	1787
aac gac aat att cca atg ctg gcc aag aaa cat gct ttt gac ata aca Asn Asp Asn Ile Pro Met Leu Ala Lys Lys His Ala Phe Asp Ile Thr 580	585	590	1835
aga gct ctc cac cat ctc tac ata tat cga gat ggc ttt agt gtt gcc Arg Ala Leu His His Leu Tyr Ile Tyr Arg Asp Gly Phe Ser Val Ala 595	600	605	1883
aac aag gaa aca aaa aaa ttg gtt atg gaa aca ctc ctt gaa tct atg Asn Lys Glu Thr Lys Lys Leu Val Met Glu Thr Leu Leu Glu Ser Met 610	615	620	1931
ctt ttt taa cta taaccatatac cataataata agctcataat gctaaattat Leu Phe			1983
tggccttatg acatagttt atgtatgtact tgtgtgaatt caatcatatc gtgtgggtat			2043
gattaaaaag ctagagctta ctaggttagt aacatggtga taaaagttat aaaatgtgag			2103
ttatagagat acccatgttg aataatgaat tacaaaaaga gaaatttatg tagaataaga			2163
ttgaaagctt ttcaattgtt taaaaaaaaaaaaaa aa			2205

<210> 32
<211> 627
<212> PRT
<213> Abies grandis

<400> 32
Met Ala Leu Val Ser Ile Ser Pro Leu Ala Ser Lys Ser Cys Leu Arg
1 5 10 15

Lys Ser Leu Ile Ser Ser Ile His Glu His Lys Pro Pro Tyr Arg Thr
20 25 30

Ile Pro Asn Leu Gly Met Arg Arg Gly Lys Ser Val Thr Pro Ser
35 40 45

Met Ser Ile Ser Leu Ala Thr Ala Ala Pro Asp Asp Gly Val Gln Arg
50 55 60

Arg Ile Gly Asp Tyr His Ser Asn Ile Trp Asp Asp Asp Phe Ile Gln
65 70 75 80

Ser Leu Ser Thr His Tyr Gly Glu Pro Ser Tyr Gln Glu Arg Ala Glu
85 90 95

Arg Leu Ile Val Glu Val Lys Lys Ile Phe Asn Ser Met Tyr Leu Asp
100 105 110

Asp Gly Arg Leu Met Ser Ser Phe Asn Asp Leu Met Gln Arg Leu Trp
115 120 125

Ile Val Asp Ser Val Glu Arg Leu Gly Ile Ala Arg His Phe Lys Asn
130 135 140

Glu Ile Thr Ser Ala Leu Asp Tyr Val Phe Arg Tyr Trp Glu Glu Asn
145 150 155 160

Gly Ile Gly Cys Gly Arg Asp Ser Ile Val Thr Asp Leu Asn Ser Thr
165 170 175

Ala Leu Gly Phe Arg Thr Leu Arg Leu His Gly Tyr Thr Val Ser Pro
180 185 190

Glu Val Leu Lys Ala Phe Gln Asp Gln Asn Gly Gln Phe Val Cys Ser
195 200 205

Pro Gly Gln Thr Glu Gly Glu Ile Arg Ser Val Leu Asn Leu Tyr Arg
210 215 220

Ala Ser Leu Ile Ala Phe Pro Gly Glu Lys Val Met Glu Glu Ala Glu
225 230 235 240

Ile Phe Ser Thr Arg Tyr Leu Lys Glu Ala Leu Gln Lys Ile Pro Val
245 250 255

Ser Ala Leu Ser Gln Glu Ile Lys Phe Val Met Glu Tyr Gly Trp His
260 265 270

Thr Asn Leu Pro Arg Leu Glu Ala Arg Asn Tyr Ile Asp Thr Leu Glu
275 280 285

Lys Asp Thr Ser Ala Trp Leu Asn Lys Asn Ala Gly Lys Lys Leu Leu
290 295 300

Glu Leu Ala Lys Leu Glu Phe Asn Ile Phe Asn Ser Leu Gln Gln Lys
305 310 315 320

Glu Leu Gln Tyr Leu Leu Arg Trp Trp Lys Glu Ser Asp Leu Pro Lys
325 330 335

Leu Thr Phe Ala Arg His Arg His Val Glu Phe Tyr Thr Leu Ala Ser
340 345 350

Cys Ile Ala Ile Asp Pro Lys His Ser Ala Phe Arg Leu Gly Phe Ala
355 360 365

Lys Met Cys His Leu Val Thr Val Leu Asp Asp Ile Tyr Asp Thr Phe
370 375 380

Gly Thr Ile Asp Glu Leu Glu Leu Phe Thr Ser Ala Ile Lys Arg Trp
385 390 395 400

Asn Ser Ser Glu Ile Glu His Leu Pro Glu Tyr Met Lys Cys Val Tyr
405 410 415

Met Val Val Phe Glu Thr Val Asn Glu Leu Thr Arg Glu Ala Glu Lys
420 425 430

Thr Gln Gly Arg Asn Thr Leu Asn Tyr Val Arg Lys Ala Trp Glu Ala
435 440 445

Tyr Phe Asp Ser Tyr Met Glu Glu Ala Lys Trp Ile Ser Asn Gly Tyr
450 455 460

Leu Pro Thr Phe Glu Glu Tyr His Glu Asn Gly Lys Val Ser Ser Ala
465 470 475 480

Tyr Arg Val Ala Thr Leu Gln Pro Ile Leu Thr Leu Asn Ala Trp Leu
485 490 495

Pro Asp Tyr Ile Leu Lys Gly Ile Asp Phe Pro Ser Arg Phe Asn Asp
500 505 510

Leu Ala Ser Ser Phe Leu Arg Leu Arg Gly Asp Thr Arg Cys Tyr Lys
515 520 525

Ala Asp Arg Asp Arg Gly Glu Glu Ala Ser Cys Ile Ser Cys Tyr Met
530 535 540

Lys Asp Asn Pro Gly Ser Thr Glu Glu Asp Ala Leu Asn His Ile Asn
545 550 555 560

Ala Met Val Asn Asp Ile Ile Lys Glu Leu Asn Trp Glu Leu Leu Arg
565 570 575

Ser Asn Asp Asn Ile Pro Met Leu Ala Lys Lys His Ala Phe Asp Ile
580 585 590

Thr Arg Ala Leu His His Leu Tyr Ile Tyr Arg Asp Gly Phe Ser Val
595 600 605

Ala Asn Lys Glu Thr Lys Lys Leu Val Met Glu Thr Leu Leu Glu Ser

610

615

620

Met Leu Phe
625

<210> 33
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR
oligonucleotide primer 2.2 BamHI

<400> 33
caaaggatc cagaatggct ctgg 24

<210> 34
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR
oligonucleotide primer 2.2 Not I

<400> 34
agtaagcgcc cgctttttaa tcataacccac 30

<210> 35
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR
oligonucleotide primer 3.18 EcoRI

<400> 35
ctgcaggaat tcggcacgag c 21

<210> 36
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR
oligonucleotide primer 3.18 SmaI

<400> 36
catagccccg ggcataatt tgagctg 27

<210> 37
<211> 30
<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR
oligonucleotide primer 10 NdeI

<400> 37

ggcaggaaca tatggctctc ctttctatcg

30

<210> 38

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR
oligonucleotide primer 10 BamHI

<400> 38

tctagaacta gtggatcccc cgggctgcag

30

<210> 39

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR
oligonucleotide primer JB29

<400> 39

ctaccattcc aatatctg

18

<210> 40

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR
oligonucleotide primer 2-8

<400> 40

gttggatctt agaagttccc

20

<210> 41

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR
oligonucleotide primer 3-9

<400> 41

tttccattcc aacctctggg

20

<210> 42
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR
oligonucleotide primer 3-11

<400> 42
cgtaatggaa agctctggcg 20

<210> 43
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR
oligonucleotide primer 7-1

<400> 43
ccttacacgc ctttggatgg 20

<210> 44
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR
oligonucleotide sequence 7-3

<400> 44
tctgttgatc caggatggtc 20

<210> 45
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: conserved
amino acid motif common to all prenyl transferases wherein Xaa at
position
3 and 4 represents any amino acid

<400> 45
Asp Asp Xaa Xaa Asp
1 5

<210> 46
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: amino acid motif from which oligonucleotide primers can be synthesized that hybridize to the monoterpene synthases of the present invention, wherein Xaa at position 4 represents
Leu or Ile or Val

<400> 46
His Ser Asn Xaa Trp Asp Asp Asp
1 5

<210> 47
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: amino acid motif from which degenerate oligonucleotides can be constructed that hybridize to the monoterpene synthases of the present invention

<400> 47
Ala Leu Asp Tyr Val Tyr
1 5

<210> 48
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: amino acid motif from which degenerate oligonucleotide sequences can be constructed that hybridize to the monoterpene synthases of the present invention

<400> 48
Glu Leu Ala Lys Leu Glu Phe
1 5

<210> 49
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: amino acid motif from which degenerate oligonucleotide sequences can be constructed that hybridize to monoterpene synthase clones of the present invention

<400> 49
Arg Trp Trp Lys Glu Ser
1 5

<210> 50
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: amino acid motif from which oligonucleotide sequences can be constructed that hybridize to monoterpene synthase clones of the present invention, wherein Xaa at position 1 represents Val or Ile or Leu

<400> 50
Xaa Leu Asp Asp Met Tyr Asp
1 5

<210> 51
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: amino acid motif from which oligonucleotide sequences can be constructed that hybridize to monoterpene synthase clones of the present invention wherein Xaa at position 1 reperesents Val or Ile or Leu

<400> 51
Xaa Leu Asp Asp Leu Tyr Asp
1 5

<210> 52
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: amino acid motif from which oligonucleotide sequences can be constructed that hybridize to the monoterpene synthase clones of the present invention, wherein Xaa at position 1 represents Val or Ile or Leu

<400> 52
Xaa Leu Asp Asp Ile Tyr Asp
1 5

<210> 53
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: amino acid

motif from which oligonucleotide sequences can be constructed that hybridize to the monoterpane synthase clones of the present invention, wherein Xaa at position 6 represents Asn or His

<400> 53
Cys Tyr Met Lys Asp Xaa Pro
1 5

<210> 54
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: exemplary oligonucleotide that corresponds to peptide sequence MetMetMet

<400> 54
atgatgatg 9

<210> 55
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: exemplary oligonucleotide sequence that corresponds to peptide sequence MetMetMet

<400> 55
tactactac 9

<210> 56
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: exemplary oligonucleotide that corresponds to peptide sequence MetMetMet, n is inosine

<400> 56
nacnacnac 9

<210> 57
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide corresponding to amino acid
sequence set forth in SEQ ID NO:46

<220>
<221> misc_feature
<222> (1)..(24)
<223> Oligonucleotide that corresponds to the conserved
amino acid sequence set forth in SEQ ID NO:46

<400> 57
gtgtcggtgg agaccctgct gctg 24

<210> 58
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide sequence corresponding to amino
acid sequence set forth in SEQ ID NO:47

<220>
<221> misc_feature
<222> (1)..(18)
<223> Oligonucleotide corresponding to amino acid
sequence set forth in SEQ ID NO:47

<400> 58
cgggagctga tgcagatg 18

<210> 59
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide that corresponds to amino acid
sequence set forth in SEQ ID NO:48

<220>
<221> misc_feature
<222> (1)..(21)
<223> Oligonucleotide that corresponds to conserved
amino acid sequence set forth in SEQ ID NO:48

<400> 59
ctcgagcggt tcgagctcaa g 21

<210> 60
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide that corresponds to amino acid
sequence set forth in SEQ ID NO:49

<220>
<221> misc_feature
<222> (1)..(18)
<223> Oligonucleotide that corresponds to conserved
amino acid sequence set forth in SEQ ID NO:49

<400> 60
gccaccaccc tcctctcg 18

<210> 61
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide sequence corresponding to amino
acid sequence set forth in SEQ ID NO:50

<220>
<221> misc_feature
<222> (1)..(21)
<223> Oligonucleotide sequence corresponding to amino
acid sequence set forth in SEQ ID NO:50

<400> 61
gaggagctgc tgtacatgct g 21

<210> 62
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide corresponding to amino acid
sequence set forth in SEQ ID NO:51

<220>
<221> misc_feature
<222> (1)..(21)
<223> Oligonucleotide corresponding to conserved amino
acid sequence set forth in SEQ ID NO:51

<400> 62
gaggagctgc tggagatgct g 21

<210> 63
<211> 293
<212> DNA
<213> Abies grandis

<400> 63
cttaatgaat tggcgcaaga ggctgagaag actcaaggca gagatacgct caactatatt 60
cgcaatgctt atgagtctca ttttgattcg tttatgcacg aagcaaaatg gatctcaagt 120

ggttatctcc caacgttga ggagtaacttg aagaatggga aagttagttc cggttctcgc 180
acagccactt tacaaccat actcaccttg gatgtaccac ttccctaatta catactgcaa 240
gaaattgatt atccatctag gttcaatgac ttggcttcgt ccctccttcg cta 293

<210> 64
<211> 2013
<212> DNA
<213> Abies grandis

<220>
<221> CDS
<222> (36)..(1889)

<400> 64
tttgacgtg ccttcttatac tgatagcaag ctgaa atg gct ctt ctt tct att 53
Met Ala Leu Leu Ser Ile
1 5

act ccg ctg gtt tcc agg tcg tgc ctc agt tct tct cat gag att aag 101
Thr Pro Leu Val Ser Arg Ser Cys Leu Ser Ser His Glu Ile Lys
10 15 20

gct ctc cgt aga aca atc cca act ctt gga atc tgc agg ccg ggg aaa 149
Ala Leu Arg Arg Thr Ile Pro Thr Leu Gly Ile Cys Arg Pro Gly Lys
25 30 35

tcc gtc gcg cat tcc ata aac atg tgt ttg aca agc gtc gca tct act 197
Ser Val Ala His Ser Ile Asn Met Cys Leu Thr Ser Val Ala Ser Thr
40 45 50

gat tct gta cag aga cgc gtg ggc aac tat cat tcc aac ctg tgg gac 245
Asp Ser Val Gln Arg Arg Val Gly Asn Tyr His Ser Asn Leu Trp Asp
55 60 65 70

gat gat ttc ata cag tct ctg atc tca acg cct tat gga gca cct gat 293
Asp Asp Phe Ile Gln Ser Leu Ile Ser Thr Pro Tyr Gly Ala Pro Asp
75 80 85

tac cgg gaa cgt gct gac aga ctt att ggg gaa gta aag gat ata atg 341
Tyr Arg Glu Arg Ala Asp Arg Leu Ile Gly Glu Val Lys Asp Ile Met
90 95 100

ttc aat ttc aag tcg ctg gaa gat gga ggc aat gat ctc ctt caa cga 389
Phe Asn Phe Lys Ser Leu Glu Asp Gly Gly Asn Asp Leu Leu Gln Arg
105 110 115

ctt ttg ctg gtc gat gac gtt gaa cgt ttg gga atc gac agg cat ttc 437
Leu Leu Leu Val Asp Asp Val Glu Arg Leu Gly Ile Asp Arg His Phe
120 125 130

aaa aaa gag ata aaa acg gca ctc gat tat gtt aac agt tat tgg aac 485
Lys Lys Glu Ile Lys Thr Ala Leu Asp Tyr Val Asn Ser Tyr Trp Asn
135 140 145 150

gaa aaa ggc att gga tgt ggg agg gag agt gtt gtg act gac ctc aac 533
Glu Lys Gly Ile Gly Cys Gly Arg Glu Ser Val Val Thr Asp Leu Asn
155 160 165

tca acc gcc ttg ggg ctt cga act ctc cga cta cac gga tac act gtg		581
Ser Thr Ala Leu Gly Leu Arg Thr Leu Arg Leu His Gly Tyr Thr Val		
170	175	180
tct tca gat gtt ttg aac gtt ttt aaa gac aaa aat ggg caa ttt tcc		629
Ser Ser Asp Val Leu Asn Val Phe Lys Asp Lys Asn Gly Gln Phe Ser		
185	190	195
tcc act gcc aat att cag ata gag gga gag att aga ggc gtt ctc aat		677
Ser Thr Ala Asn Ile Gln Ile Glu Gly Glu Ile Arg Gly Val Leu Asn		
200	205	210
tta ttc agg gcc tcc ctc gtc gcc ttt ccc ggc gag aaa gtt atg gat		725
Leu Phe Arg Ala Ser Leu Val Ala Phe Pro Gly Glu Lys Val Met Asp		
215	220	225
230		
gaa gct gaa aca ttc tct aca aaa tat tta aga gaa gcc ctg caa aag		773
Glu Ala Glu Thr Phe Ser Thr Lys Tyr Leu Arg Glu Ala Leu Gln Lys		
235	240	245
att ccg gca tcc agt ata ctt tca cta gag ata cgg gac gtt ctg gaa		821
Ile Pro Ala Ser Ser Ile Leu Ser Leu Glu Ile Arg Asp Val Leu Glu		
250	255	260
265	270	275
tat ggt tgg cac acc aat ttg cca cgc ttg gaa gca agg aat tac atg		869
Tyr Gly Trp His Thr Asn Leu Pro Arg Leu Glu Ala Arg Asn Tyr Met		
280	285	290
295	300	305
310		
aga gag tta aaa cat gtt tcc cga tgg tgg aaa gac tcg ggt tct cct		1013
Arg Glu Leu Lys His Val Ser Arg Trp Trp Lys Asp Ser Gly Ser Pro		
315	320	325
330	335	340
345	350	355
acc aag atg tct cat ctt atc acg gtt ctt gac gac atg tac gac gtc		1157
Thr Lys Met Ser His Leu Ile Thr Val Leu Asp Asp Met Tyr Asp Val		
360	365	370
375	380	385
390		
tgg gat ccg tcc gcg atg gaa tgc ctt cca gaa tat atg aaa gga gtg		1253
Trp Asp Pro Ser Ala Met Glu Cys Leu Pro Glu Tyr Met Lys Gly Val		
395	400	405
tac atg atg gtt tat cac acc gta aat gaa atg gct cga gtg gca gag		1301

Tyr Met Met Val Tyr His Thr Val Asn Glu Met Ala Arg Val Ala Glu
410 415 420

aag gct caa ggc cga gac acg ctc aac tat gca aga cag gct tgg gag 1349
Lys Ala Gln Gly Arg Asp Thr Leu Asn Tyr Ala Arg Gln Ala Trp Glu
425 430 435

gcg tgt ttt gat tcg tat atg cag gaa gca aag tgg atc gcc act ggt 1397
Ala Cys Phe Asp Ser Tyr Met Gln Glu Ala Lys Trp Ile Ala Thr Gly
440 445 450

tat ctg ccc acg ttt gag gag tac ttg gag aac ggg aaa gtt agc tct 1445
Tyr Leu Pro Thr Phe Glu Glu Tyr Leu Glu Asn Gly Lys Val Ser Ser
455 460 465 470

gct cat cgc cca tgc gca ctg caa ccc att ctg acg ttg gac atc ccc 1493
Ala His Arg Pro Cys Ala Leu Gln Pro Ile Leu Thr Leu Asp Ile Pro
475 480 485

ttt cct gat cac atc ctc aag gaa gtt gac ttc cca tcg aag ctc aat 1541
Phe Pro Asp His Ile Leu Lys Glu Val Asp Phe Pro Ser Lys Leu Asn
490 495 500

gac ttg ata tgt atc atc ctt cga tta aga ggt gat aca cgg tgc tac 1589
Asp Leu Ile Cys Ile Ile Leu Arg Leu Arg Gly Asp Thr Arg Cys Tyr
505 510 515

aag gca gac agg gcc cgt gga gaa gaa gct tcg tct ata tca tgt tat 1637
Lys Ala Asp Arg Ala Arg Gly Glu Glu Ala Ser Ser Ile Ser Cys Tyr
520 525 530

atg aaa gac aat cct gga tta acg gaa gaa gat gct ctg aat cat atc 1685
Met Lys Asp Asn Pro Gly Leu Thr Glu Glu Asp Ala Leu Asn His Ile
535 540 545 550

aac ttc atg atc agg gac gca atc aga gaa tta aat tgg gag ctt cta 1733
Asn Phe Met Ile Arg Asp Ala Ile Arg Glu Leu Asn Trp Glu Leu Leu
555 560 565

aag cca gac aac agt gtt ccc atc act tcc aag aaa cac gca ttt gac 1781
Lys Pro Asp Asn Ser Val Pro Ile Thr Ser Lys Lys His Ala Phe Asp
570 575 580

ata agc aga gtt tgg cat cac ggt tac aga tac cga gat ggc tac agc 1829
Ile Ser Arg Val Trp His His Gly Tyr Arg Tyr Arg Asp Gly Tyr Ser
585 590 595

ttt gcc aac gtt gaa aca aag agt ttg gtg atg aga acc gtc att gaa 1877
Phe Ala Asn Val Glu Thr Lys Ser Leu Val Met Arg Thr Val Ile Glu
600 605 610

cct gtg cct ttg taacaacact tcaaattcac aatattaact gaggatgcc 1929
Pro Val Pro Leu
615

tatgggtgta tatagggcac acaaaaataa atatggttgt gtttagtaaag ctgtaattta 1989

tgaaaaaaaaaaaaaaa aaaaaaaa 2013

<211> 618
<212> PRT
<213> Abies grandis

<400> 65
Met Ala Leu Leu Ser Ile Thr Pro Leu Val Ser Arg Ser Cys Leu Ser
1 5 10 15

Ser Ser His Glu Ile Lys Ala Leu Arg Arg Thr Ile Pro Thr Leu Gly
20 25 30

Ile Cys Arg Pro Gly Lys Ser Val Ala His Ser Ile Asn Met Cys Leu
35 40 45

Thr Ser Val Ala Ser Thr Asp Ser Val Gln Arg Arg Val Gly Asn Tyr
50 55 60

His Ser Asn Leu Trp Asp Asp Asp Phe Ile Gln Ser Leu Ile Ser Thr
65 70 75 80

Pro Tyr Gly Ala Pro Asp Tyr Arg Glu Arg Ala Asp Arg Leu Ile Gly
85 90 95

Glu Val Lys Asp Ile Met Phe Asn Phe Lys Ser Leu Glu Asp Gly Gly
100 105 110

Asn Asp Leu Leu Gln Arg Leu Leu Val Asp Asp Val Glu Arg Leu
115 120 125

Gly Ile Asp Arg His Phe Lys Lys Glu Ile Lys Thr Ala Leu Asp Tyr
130 135 140

Val Asn Ser Tyr Trp Asn Glu Lys Gly Ile Gly Cys Gly Arg Glu Ser
145 150 155 160

Val Val Thr Asp Leu Asn Ser Thr Ala Leu Gly Leu Arg Thr Leu Arg
165 170 175

Leu His Gly Tyr Thr Val Ser Ser Asp Val Leu Asn Val Phe Lys Asp
180 185 190

Lys Asn Gly Gln Phe Ser Ser Thr Ala Asn Ile Gln Ile Glu Gly Glu
195 200 205

Ile Arg Gly Val Leu Asn Leu Phe Arg Ala Ser Leu Val Ala Phe Pro
210 215 220

Gly Glu Lys Val Met Asp Glu Ala Glu Thr Phe Ser Thr Lys Tyr Leu
225 230 235 240

Arg Glu Ala Leu Gln Lys Ile Pro Ala Ser Ser Ile Leu Ser Leu Glu
245 250 255

Ile Arg Asp Val Leu Glu Tyr Gly Trp His Thr Asn Leu Pro Arg Leu
260 265 270

Glu Ala Arg Asn Tyr Met Asp Val Phe Gly Gln His Thr Lys Asn Lys
275 280 285

Asn Ala Ala Glu Lys Leu Leu Glu Leu Ala Lys Leu Glu Phe Asn Ile
290 295 300

Phe His Ser Leu Gln Glu Arg Glu Leu Lys His Val Ser Arg Trp Trp
305 310 315 320

Lys Asp Ser Gly Ser Pro Glu Met Thr Phe Cys Arg His Arg His Val
325 330 335

Glu Tyr Tyr Ala Leu Ala Ser Cys Ile Ala Phe Glu Pro Gln His Ser
340 345 350

Gly Phe Arg Leu Gly Phe Thr Lys Met Ser His Leu Ile Thr Val Leu
355 360 365

Asp Asp Met Tyr Asp Val Phe Gly Thr Val Asp Glu Leu Glu Leu Phe
370 375 380

Thr Ala Thr Ile Lys Arg Trp Asp Pro Ser Ala Met Glu Cys Leu Pro
385 390 395 400

Glu Tyr Met Lys Gly Val Tyr Met Met Val Tyr His Thr Val Asn Glu
405 410 415

Met Ala Arg Val Ala Glu Lys Ala Gln Gly Arg Asp Thr Leu Asn Tyr
420 425 430

Ala Arg Gln Ala Trp Glu Ala Cys Phe Asp Ser Tyr Met Gln Glu Ala
435 440 445

Lys Trp Ile Ala Thr Gly Tyr Leu Pro Thr Phe Glu Glu Tyr Leu Glu
450 455 460

Asn Gly Lys Val Ser Ser Ala His Arg Pro Cys Ala Leu Gln Pro Ile
465 470 475 480

Leu Thr Leu Asp Ile Pro Phe Pro Asp His Ile Leu Lys Glu Val Asp
485 490 495

Phe Pro Ser Lys Leu Asn Asp Leu Ile Cys Ile Ile Leu Arg Leu Arg
500 505 510

Gly Asp Thr Arg Cys Tyr Lys Ala Asp Arg Ala Arg Gly Glu Glu Ala
515 520 525

Ser Ser Ile Ser Cys Tyr Met Lys Asp Asn Pro Gly Leu Thr Glu Glu
530 535 540

Asp Ala Leu Asn His Ile Asn Phe Met Ile Arg Asp Ala Ile Arg Glu
545 550 555 560

Leu Asn Trp Glu Leu Leu Lys Pro Asp Asn Ser Val Pro Ile Thr Ser
565 570 575

Lys Lys His Ala Phe Asp Ile Ser Arg Val Trp His His Gly Tyr Arg
580 585 590

Tyr Arg Asp Gly Tyr Ser Phe Ala Asn Val Glu Thr Lys Ser Leu Val
595 600 605

Met Arg Thr Val Ile Glu Pro Val Pro Leu
610 615

<210> 66
<211> 2186
<212> DNA
<213> Abies grandis

<220>
<221> CDS
<222> (34)..(1923)

<400> 66
cccaaatcct atatccgtta taagcgagca gga atg gct ctg gtt tct tcc gca 54
Met Ala Leu Val Ser Ser Ala
1 5

ccc aaa tcc tgc ctg cac aaa tcg ttg atc agg tct act cat cat gag 102
Pro Lys Ser Cys Leu His Lys Ser Leu Ile Arg Ser Thr His His Glu
10 15 20

ctc aag cct ctg cgc aga acc atc cca act ctt gga atg tgt agg cga 150
Leu Lys Pro Leu Arg Arg Thr Ile Pro Thr Leu Gly Met Cys Arg Arg
25 30 35

ggg aaa tct ttc aca cct tct gtg agc atg agt ttg acc acc gct gta 198
Gly Lys Ser Phe Thr Pro Ser Val Ser Met Ser Leu Thr Thr Ala Val
40 45 50 55

tct gat gat ggt cta caa aga cgc ata ggt gac tat cat tcc aat ctc 246
Ser Asp Asp Gly Leu Gln Arg Arg Ile Gly Asp Tyr His Ser Asn Leu
60 65 70

tgg gac gac gat ttc ata cag tct cta tca acg cct tat ggg gag cct 294
Trp Asp Asp Asp Phe Ile Gln Ser Leu Ser Thr Pro Tyr Gly Glu Pro
75 80 85

tct tac cga gaa cgt gct gag aaa ctg att ggg gaa gtg aag gag atg 342
Ser Tyr Arg Glu Arg Ala Glu Lys Leu Ile Gly Glu Val Lys Glu Met
90 95 100

ttc aat tca atg cca tcg gaa gat gga gaa tca atg agt ccc ctc aat 390
Phe Asn Ser Met Pro Ser Glu Asp Gly Glu Ser Met Ser Pro Leu Asn
105 110 115

gat ctt att gaa cga ctt tgg atg gtc gat agc gtt gaa cgt ttg ggg 438
Asp Leu Ile Glu Arg Leu Trp Met Val Asp Ser Val Glu Arg Leu Gly
120 125 130 135

att gat aga cat ttc aaa aaa gag ata aaa tca gcc ctt gat tat gtt 486
Ile Asp Arg His Phe Lys Lys Glu Ile Lys Ser Ala Leu Asp Tyr Val
140 145 150

tac agt tat tgg aac gaa aaa ggt att gga tgc ggt aga gat agt gtt 534
Tyr Ser Tyr Trp Asn Glu Lys Gly Ile Gly Cys Gly Arg Asp Ser Val
155 160 165

ttt cct gat gtc aac tcg act gcc tcg ggg ttt cga act ctt cgc cta 582
Phe Pro Asp Val Asn Ser Thr Ala Ser Gly Phe Arg Thr Leu Arg Leu
170 175 180

cac gga tac agt gtc tct tca gag gtt ttg aaa gta ttt caa gac caa 630
His Gly Tyr Ser Val Ser Ser Glu Val Leu Lys Val Phe Gln Asp Gln

185	190	195														
aat	ggg	cag	ttt	gca	tcc	tct	cct	agt	aca	aaa	gag	aga	gac	atc	aga	678
Asn	Gly	Gln	Phe	Ala	Phe	Ser	Pro	Ser	Thr	Lys	Glu	Arg	Asp	Ile	Arg	
200				205					210					215		
acc	gtt	ctg	aat	tta	tat	cgg	gct	tct	ttc	att	gcc	ttt	cct	ggg	gag	726
Thr	Val	Leu	Asn	Leu	Tyr	Arg	Ala	Ser	Phe	Ile	Ala	Phe	Pro	Gly	Glu	
220					225					230						
aaa	gtt	atg	gaa	gag	gct	gaa	att	ttc	tct	tca	aga	tat	ttg	aaa	gaa	774
Lys	Val	Met	Glu	Glu	Ala	Glu	Ile	Phe	Ser	Ser	Arg	Tyr	Leu	Lys	Glu	
235					240					245						
gcc	gtg	caa	aag	att	ccg	gtc	tcc	agt	ctt	tca	caa	gaa	ata	gac	tac	822
Ala	Val	Gln	Lys	Ile	Pro	Val	Ser	Ser	Leu	Ser	Gln	Glu	Ile	Asp	Tyr	
250					255					260						
act	ttg	gaa	tat	ggt	tgg	cac	aca	aat	atg	cca	aga	ttg	gaa	aca	agg	870
Thr	Leu	Glu	Tyr	Gly	Trp	His	Thr	Asn	Met	Pro	Arg	Leu	Glu	Thr	Arg	
265					270				275							
aat	tac	tta	gat	gta	ttt	gga	cat	cct	acc	agt	cca	tgg	ctc	aag	aag	918
Asn	Tyr	Leu	Asp	Val	Phe	Gly	His	Pro	Thr	Ser	Pro	Trp	Leu	Lys	Lys	
280					285				290				295			
aaa	agg	acg	caa	tat	ctg	gac	agc	gaa	aag	ctt	tta	gaa	ctc	gca	aaa	966
Lys	Arg	Thr	Gln	Tyr	Leu	Asp	Ser	Glu	Lys	Leu	Leu	Glu	Leu	Ala	Lys	
300					305				310							
ttg	gag	ttc	aac	atc	ttt	cac	tcc	ctt	caa	cag	aag	gag	tta	cag	tat	1014
Leu	Glu	Phe	Asn	Ile	Phe	His	Ser	Leu	Gln	Gln	Lys	Glu	Leu	Gln	Tyr	
315					320				325							
ctc	tcc	aga	tgg	tgg	ata	cat	tcg	ggt	ttg	cct	gaa	ctg	acc	ttt	ggt	1062
Leu	Ser	Arg	Trp	Trp	Ile	His	Ser	Gly	Leu	Pro	Glu	Leu	Thr	Phe	Gly	
330					335				340							
cgg	cat	cgt	cac	gtg	gaa	tac	tac	acc	ctg	agc	tct	tgc	att	gcg	act	1110
Arg	His	Arg	His	Val	Glu	Tyr	Tyr	Thr	Leu	Ser	Ser	Cys	Ile	Ala	Thr	
345					350				355							
gag	ccc	aaa	cat	tct	gca	ttc	aga	ttg	ggc	ttt	gcc	aaa	acg	tgt	cat	1158
Glu	Pro	Lys	His	Ser	Ala	Phe	Arg	Leu	Gly	Phe	Ala	Lys	Thr	Cys	His	
360					365				370			375				
ctt	atc	acg	gtt	ctg	gac	gat	atc	tac	gac	act	ttc	gga	acg	atg	gat	1206
Leu	Ile	Thr	Val	Leu	Asp	Asp	Ile	Tyr	Asp	Thr	Phe	Gly	Thr	Met	Asp	
380					385				390							
gaa	atc	gaa	ctc	ttc	aac	gag	gca	gtt	agg	aga	tgg	aat	ccg	tcg	gag	1254
Glu	Ile	Glu	Leu	Phe	Asn	Glu	Ala	Val	Arg	Arg	Trp	Asn	Pro	Ser	Glu	
395					400				405							
aaa	gaa	cgc	ctc	cca	gaa	tat	atg	aaa	gaa	atc	tac	atg	gca	ctc	tac	1302
Lys	Glu	Arg	Leu	Pro	Glu	Tyr	Met	Lys	Glu	Ile	Tyr	Met	Ala	Leu	Tyr	
410					415				420							
gaa	gcc	tta	act	gac	atg	gcg	cga	gag	gca	gag	aag	aca	caa	ggc	cga	1350
Glu	Ala	Leu	Thr	Asp	Met	Ala	Arg	Glu	Ala	Glu	Lys	Thr	Gln	Gly	Arg	
425					430				435							

gac acg ctc aat tat gct aga aag gct tgg gaa gtt tat ctt gat tcg 1398
Asp Thr Leu Asn Tyr Ala Arg Lys Ala Trp Glu Val Tyr Leu Asp Ser
440 445 450 455

tat aca caa gaa gca aag tgg atc gcc agc ggt tat ctg cca act ttc 1446
Tyr Thr Gln Glu Ala Lys Trp Ile Ala Ser Gly Tyr Leu Pro Thr Phe
460 465 470

gag gag tac tta gag aac gcg aag gtt agc tct ggt cat cgt gca gcg 1494
Glu Glu Tyr Leu Glu Asn Ala Lys Val Ser Ser Gly His Arg Ala Ala
475 480 485

gca ttg aca ccc ctc ctg aca ttg gac gta ccg ctt cct gat gac gtc 1542
Ala Leu Thr Pro Leu Leu Thr Leu Asp Val Pro Leu Pro Asp Asp Val
490 495 500

ttg aag gga ata gat ttt cca tcg aga ttt aat gat ttg gca tct tcc 1590
Leu Lys Gly Ile Asp Phe Pro Ser Arg Phe Asn Asp Leu Ala Ser Ser
505 510 515

tcc ctt aga cta aga ggt gac aca cga tgc tac aag gca gac agg gac 1638
Phe Leu Arg Leu Arg Gly Asp Thr Arg Cys Tyr Lys Ala Asp Arg Asp
520 525 530 535

cga gga gaa gaa gcg tca agc ata tcg tgt tac atg aaa gac aat ccc 1686
Arg Gly Glu Glu Ala Ser Ser Ile Ser Cys Tyr Met Lys Asp Asn Pro
540 545 550

gga tta aca gag gaa gat gct ctc aat cat atc aat gcc atg atc aac 1734
Gly Leu Thr Glu Glu Asp Ala Leu Asn His Ile Asn Ala Met Ile Asn
555 560 565

gac ata atc aaa gaa tta aat tgg gaa ctt ctc aaa ccc gat agc aat 1782
Asp Ile Ile Lys Glu Leu Asn Trp Glu Leu Leu Lys Pro Asp Ser Asn
570 575 580

att cca atg act gca cgg aaa cat gct tat gag ata acc aga gct ttc 1830
Ile Pro Met Thr Ala Arg Lys His Ala Tyr Glu Ile Thr Arg Ala Phe
585 590 595

cac caa ctt tac aaa tat aga gat ggc ttc agc gtt gcc act caa gaa 1878
His Gln Leu Tyr Lys Tyr Arg Asp Gly Phe Ser Val Ala Thr Gln Glu
600 605 610 615

acg aaa agt ttg gtg agg aga acg gtc ctt gaa cca gtg cct ctt 1923
Thr Lys Ser Leu Val Arg Arg Thr Val Leu Glu Pro Val Pro Leu
620 625 630

taacaattta aaccttctat aataaattgg tgtaggctcc gctatgcgtt tatgcatttg 1983
catgtctctc tatgtacta gttgtatgcg tggatgatt ataaaattgg aggttactcg 2043
gtcctcacat ggtaatatgt gagttgtgaa attctcaaaa aaaaaaaaaa aaaaaaaaaa 2103
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2163
aaaaaaaaaa aaaaaaaaaa aaa 2186

<211> 630

<212> PRT

<213> Abies grandis

<400> 67

Met Ala Leu Val Ser Ser Ala Pro Lys Ser Cys Leu His Lys Ser Leu
1 5 10 15

Ile Arg Ser Thr His His Glu Leu Lys Pro Leu Arg Arg Thr Ile Pro
20 25 30

Thr Leu Gly Met Cys Arg Arg Gly Lys Ser Phe Thr Pro Ser Val Ser
35 40 45

Met Ser Leu Thr Thr Ala Val Ser Asp Asp Gly Leu Gln Arg Arg Ile
50 55 60

Gly Asp Tyr His Ser Asn Leu Trp Asp Asp Asp Phe Ile Gln Ser Leu
65 70 75 80

Ser Thr Pro Tyr Gly Glu Pro Ser Tyr Arg Glu Arg Ala Glu Lys Leu
85 90 95

Ile Gly Glu Val Lys Glu Met Phe Asn Ser Met Pro Ser Glu Asp Gly
100 105 110

Glu Ser Met Ser Pro Leu Asn Asp Leu Ile Glu Arg Leu Trp Met Val
115 120 125

Asp Ser Val Glu Arg Leu Gly Ile Asp Arg His Phe Lys Lys Glu Ile
130 135 140

Lys Ser Ala Leu Asp Tyr Val Tyr Ser Tyr Trp Asn Glu Lys Gly Ile
145 150 155 160

Gly Cys Gly Arg Asp Ser Val Phe Pro Asp Val Asn Ser Thr Ala Ser
165 170 175

Gly Phe Arg Thr Leu Arg Leu His Gly Tyr Ser Val Ser Ser Glu Val
180 185 190

Leu Lys Val Phe Gln Asp Gln Asn Gly Gln Phe Ala Phe Ser Pro Ser
195 200 205

Thr Lys Glu Arg Asp Ile Arg Thr Val Leu Asn Leu Tyr Arg Ala Ser
210 215 220

Phe Ile Ala Phe Pro Gly Glu Lys Val Met Glu Glu Ala Glu Ile Phe
225 230 235 240

Ser Ser Arg Tyr Leu Lys Glu Ala Val Gln Lys Ile Pro Val Ser Ser
245 250 255

Leu Ser Gln Glu Ile Asp Tyr Thr Leu Glu Tyr Gly Trp His Thr Asn
260 265 270

Met Pro Arg Leu Glu Thr Arg Asn Tyr Leu Asp Val Phe Gly His Pro
275 280 285

Thr Ser Pro Trp Leu Lys Lys Lys Arg Thr Gln Tyr Leu Asp Ser Glu
290 295 300

Lys Leu Leu Glu Leu Ala Lys Leu Glu Phe Asn Ile Phe His Ser Leu
305 310 315 320

Gln Gln Lys Glu Leu Gln Tyr Leu Ser Arg Trp Trp Ile His Ser Gly
325 330 335

Leu Pro Glu Leu Thr Phe Gly Arg His Arg His Val Glu Tyr Tyr Thr
340 345 350

Leu Ser Ser Cys Ile Ala Thr Glu Pro Lys His Ser Ala Phe Arg Leu
355 360 365

Gly Phe Ala Lys Thr Cys His Leu Ile Thr Val Leu Asp Asp Ile Tyr
370 375 380

Asp Thr Phe Gly Thr Met Asp Glu Ile Glu Leu Phe Asn Glu Ala Val
385 390 395 400

Arg Arg Trp Asn Pro Ser Glu Lys Glu Arg Leu Pro Glu Tyr Met Lys
405 410 415

Glu Ile Tyr Met Ala Leu Tyr Glu Ala Leu Thr Asp Met Ala Arg Glu
420 425 430

Ala Glu Lys Thr Gln Gly Arg Asp Thr Leu Asn Tyr Ala Arg Lys Ala
435 440 445

Trp Glu Val Tyr Leu Asp Ser Tyr Thr Gln Glu Ala Lys Trp Ile Ala
450 455 460

Ser Gly Tyr Leu Pro Thr Phe Glu Glu Tyr Leu Glu Asn Ala Lys Val
465 470 475 480

Ser Ser Gly His Arg Ala Ala Leu Thr Pro Leu Leu Thr Leu Asp
485 490 495

Val Pro Leu Pro Asp Asp Val Leu Lys Gly Ile Asp Phe Pro Ser Arg
500 505 510

Phe Asn Asp Leu Ala Ser Ser Phe Leu Arg Leu Arg Gly Asp Thr Arg
515 520 525

Cys Tyr Lys Ala Asp Arg Asp Arg Gly Glu Glu Ala Ser Ser Ile Ser
530 535 540

Cys Tyr Met Lys Asp Asn Pro Gly Leu Thr Glu Glu Asp Ala Leu Asn
545 550 555 560

His Ile Asn Ala Met Ile Asn Asp Ile Ile Lys Glu Leu Asn Trp Glu
565 570 575

Leu Leu Lys Pro Asp Ser Asn Ile Pro Met Thr Ala Arg Lys His Ala
580 585 590

Tyr Glu Ile Thr Arg Ala Phe His Gln Leu Tyr Lys Tyr Arg Asp Gly
595 600 605

Phe Ser Val Ala Thr Gln Glu Thr Lys Ser Leu Val Arg Arg Thr Val
610 615 620

Leu Glu Pro Val Pro Leu
625 630

<210> 68
<211> 2429

<212> DNA

<213> Abies grandis

<220>

<221> CDS

<222> (35)..(1945)

<400> 68

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Met Ala Leu Leu Ser Ile Val
1 5

tct ttg cag gtt ccc aaa tcc tgc ggg ctg aaa tcg ttg atc agt tcc 103
Ser Leu Gln Val Pro Lys Ser Cys Gly Leu Lys Ser Leu Ile Ser Ser
10 15 20

agc aat gtg cag aag gct ctc tgt atc tct aca gca gtc cca act ctc 151
Ser Asn Val Gln Lys Ala Leu Cys Ile Ser Thr Ala Val Pro Thr Leu
25 30 35

aga atg cgt agg cga cag aaa gct ctg gtc atc aac atg aaa ttg acc 199
Arg Met Arg Arg Gln Lys Ala Leu Val Ile Asn Met Lys Leu Thr
40 45 50 55

act gta tcc cat cgt gat gat aat ggt ggt gta ctg caa aga cgc 247
Thr Val Ser His Arg Asp Asp Asn Gly Gly Val Leu Gln Arg Arg
60 65 70

ata gcc gat cat cat ccc aac ctg tgg gaa gat gat ttc ata caa tca 295
Ile Ala Asp His His Pro Asn Leu Trp Glu Asp Asp Phe Ile Gln Ser
75 80 85

ttg tcc tca cct tat ggg gga tct tcg tac agt gaa cgt gct gtg aca 343
Leu Ser Ser Pro Tyr Gly Gly Ser Ser Tyr Ser Glu Arg Ala Val Thr
90 95 100

gtg gtt gag gaa gta aaa gag atg ttc aat tca ata cca aat aat aga 391
Val Val Glu Glu Val Lys Glu Met Phe Asn Ser Ile Pro Asn Asn Arg
105 110 115

gaa tta ttt ggt tcc caa aat gat ctc ctt aca cgc ctt tgg atg gtg 439
Glu Leu Phe Gly Ser Gln Asn Asp Leu Leu Thr Arg Leu Trp Met Val
120 125 130 135

gat agc att gaa cgt ctg ggg ata gat aga cat ttc caa aat gag ata 487
Asp Ser Ile Glu Arg Leu Gly Ile Asp Arg His Phe Gln Asn Glu Ile
140 145 150

aga gta gcc ctc gat tat gtt tac agt tat tgg aag gaa aag gaa ggc 535
Arg Val Ala Leu Asp Tyr Val Tyr Ser Tyr Trp Lys Glu Lys Glu Gly
155 160 165

att ggg tgt ggc aga gat tct act ttt cct gat ctc aac tcg act gct 583
Ile Gly Cys Gly Arg Asp Ser Thr Phe Pro Asp Leu Asn Ser Thr Ala
170 175 180

ctg gcg ctt cga act ctt cga ctg cac gga tac aat gtg tct tca gat 631
 Leu Ala Leu Arg Thr Leu Arg Leu His Gly Tyr Asn Val Ser Ser Asp
 185 190 195

 gtg ctg gaa tac ttc aaa gat caa aag ggg cat ttt gcc tgc cct gca 679
 Val Leu Glu Tyr Phe Lys Asp Gln Lys Gly His Phe Ala Cys Pro Ala
 200 205 210 215

 atc cta acc gag gga cag atc act aga agt gtt cta aat tta tat cgg 727
 Ile Leu Thr Glu Gly Gln Ile Thr Arg Ser Val Leu Asn Leu Tyr Arg
 220 225 230

 gct tcc ctg gtc gcc ttt ccg ggg gag aaa gtt atg gaa gag gct gaa 775
 Ala Ser Leu Val Ala Phe Pro Gly Glu Lys Val Met Glu Glu Ala Glu
 235 240 245

 atc ttc tcg gca tct tat ttg aaa gaa gtc tta caa aag att cca gtc 823
 Ile Phe Ser Ala Ser Tyr Leu Lys Glu Val Leu Gln Lys Ile Pro Val
 250 255 260

 tcc agt ttt tca cga gag ata gaa tac gtt ttg gaa tat ggt tgg cac 871
 Ser Ser Phe Ser Arg Glu Ile Glu Tyr Val Leu Glu Tyr Gly Trp His
 265 270 275

 aca aat ttg cca aga ttg gaa gca aga aat tat atc gac gtc tac ggg 919
 Thr Asn Leu Pro Arg Leu Glu Ala Arg Asn Tyr Ile Asp Val Tyr Gly
 280 285 290 295

 cag gac agc tat gaa agt tca aac gag atg cca tat gtg aat acg cag 967
 Gln Asp Ser Tyr Glu Ser Ser Asn Glu Met Pro Tyr Val Asn Thr Gln
 300 305 310

 aag ctt tta aaa ctt gca aaa ttg gag ttt aat atc ttt cac tct ttg 1015
 Lys Leu Leu Lys Leu Ala Lys Leu Glu Phe Asn Ile Phe His Ser Leu
 315 320 325

 caa cag aaa gag ttg caa tat atc tct aga tgg tgg aaa gat tcg tgt 1063
 Gln Gln Lys Glu Leu Gln Tyr Ile Ser Arg Trp Trp Lys Asp Ser Cys
 330 335 340

 tca tct cat ctg act ttt act cga cac cgt cac gtg gaa tac tac aca 1111
 Ser Ser His Leu Thr Phe Thr Arg His Arg His Val Glu Tyr Tyr Thr
 345 350 355

 atg gca tct tgc att tct atg gag ccg aaa cac tcc gct ttc aga ttg 1159
 Met Ala Ser Cys Ile Ser Met Glu Pro Lys His Ser Ala Phe Arg Leu
 360 365 370 375

 ggg ttt gtc aaa aca tgt cat ctt cta aca gtt ctg gat gat atg tat 1207
 Gly Phe Val Lys Thr Cys His Leu Leu Thr Val Leu Asp Asp Met Tyr
 380 385 390

 gac act ttt gga aca ctg gac gaa ctc caa ctt ttt acg act gcc ttt 1255
 Asp Thr Phe Gly Thr Leu Asp Glu Leu Gln Leu Phe Thr Thr Ala Phe
 395 400 405

 aag aca tgg gat ttg tca gag aca aag tgt ctt cca gaa tat atg aaa 1303
 Lys Arg Trp Asp Leu Ser Glu Thr Lys Cys Leu Pro Glu Tyr Met Lys
 410 415 420

gca gtg tac atg gac ttg tat caa tgt ctt aat gaa ttg gcg caa gag 1351
Ala Val Tyr Met Asp Leu Tyr Gln Cys Leu Asn Glu Leu Ala Gln Glu
425 430 435

gct gag aag act caa ggc aga gat acg ctc aac tat att cgc aat gct 1399
Ala Glu Lys Thr Gln Gly Arg Asp Thr Leu Asn Tyr Ile Arg Asn Ala
440 445 450 455

tat gag tct cat ttt gat tcg ttt atg cac gaa gca aaa tgg atc tca 1447
Tyr Glu Ser His Phe Asp Ser Phe Met His Glu Ala Lys Trp Ile Ser
460 465 470

agt ggt tat ctc cca acg ttt gag gag tac ttg aag aat ggg aaa gtt 1495
Ser Gly Tyr Leu Pro Thr Phe Glu Glu Tyr Leu Lys Asn Gly Lys Val
475 480 485

agt tcc ggt tct cgc aca gcc act tta caa ccc ata ctc acc ttg gat 1543
Ser Ser Gly Ser Arg Thr Ala Thr Leu Gln Pro Ile Leu Thr Leu Asp
490 495 500

gta cca ctt cct aat tac ata ctg caa gaa att gat tat cca tct agg 1591
Val Pro Leu Pro Asn Tyr Ile Leu Gln Glu Ile Asp Tyr Pro Ser Arg
505 510 515

ttc aat gac ttg gct tcg tcc ctc ctt cg^g cta cgt ggt gac acg cgc 1639
Phe Asn Asp Leu Ala Ser Ser Leu Leu Arg Leu Arg Gly Asp Thr Arg
520 525 530 535

tgc tac aag gcg gat agg gct cgt gga gaa gaa gct tca gct ata tcg 1687
Cys Tyr Lys Ala Asp Arg Ala Arg Gly Glu Glu Ala Ser Ala Ile Ser
540 545 550

tgt tat atg aaa gac cat cct gga tca aca gag gaa gat gct ctc aat 1735
Cys Tyr Met Lys Asp His Pro Gly Ser Thr Glu Glu Asp Ala Leu Asn
555 560 565

cat atc aac gtc atg atc agt gat gca atc aga gaa tta aat tgg gag 1783
His Ile Asn Val Met Ile Ser Asp Ala Ile Arg Glu Leu Asn Trp Glu
570 575 580

ctt ctc aga cca gat agc aaa agt ccc atc tct tcc aag aaa cat gct 1831
Leu Leu Arg Pro Asp Ser Lys Ser Pro Ile Ser Ser Lys Lys His Ala
585 590 595

ttt gac atc acc aga gct ttc cat cac ctc tac aag tac cga gat ggt 1879
Phe Asp Ile Thr Arg Ala Phe His His Leu Tyr Lys Tyr Arg Asp Gly
600 605 610 615

tac act gtt gcg agt agt gaa aca aag aat ttg gtg atg aaa aca gtt 1927
Tyr Thr Val Ala Ser Ser Glu Thr Lys Asn Leu Val Met Lys Thr Val
620 625 630

ctt gaa cct gtg gca ttg taaaaaata tcaaccgcataaaaatgcac 1975
Leu Glu Pro Val Ala Leu
635

ggagtttgta atttaatgca cttctttat aatacacttc tcttagacc tgtagtgaag 2035
ccgatgcacc attacagtgt atatggagc cagtcgttc tcaaaaagtt tgtaaatgtt 2095
attctatgtt atactcttta gacaaaagc tagatgccca tgaaaagcaa gtgttttaga 2155

attgcttctg gatttgctta aattttctcc atgattcttt agaaatgttg catccccaaa 2215
cttcactgcc atataagata acgggagtga caaggatttt aaagaggatt ttttttatg 2275
tcccgcatca caaggtttgt cgatttacag ttgtttcaa gactgaagta ggatttccac 2335
cctccattaa tcctcttctc gatgttata tag tttcacttga gcttgtgatg gaagtcaatt 2395
cctagatatt tataagaaaa aaaaaaaaaa aaaa 2429

<210> 69
<211> 637
<212> PRT
<213> Abies grandis

<400> 69
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Leu Lys Ser Leu Ile Ser Ser Ser Asn Val Gln Lys Ala Leu Cys Ile
20 25 30

Ser Thr Ala Val Pro Thr Leu Arg Met Arg Arg Arg Gln Lys Ala Leu
35 40 45

Val Ile Asn Met Lys Leu Thr Thr Val Ser His Arg Asp Asp Asn Gly
50 55 60

Gly Gly Val Leu Gln Arg Arg Ile Ala Asp His His Pro Asn Leu Trp
65 70 75 80

Glu Asp Asp Phe Ile Gln Ser Leu Ser Ser Pro Tyr Gly Ser Ser
85 90 95

Tyr Ser Glu Arg Ala Val Thr Val Val Glu Glu Val Lys Glu Met Phe
100 105 110

Asn Ser Ile Pro Asn Asn Arg Glu Leu Phe Gly Ser Gln Asn Asp Leu
115 120 125

Leu Thr Arg Leu Trp Met Val Asp Ser Ile Glu Arg Leu Gly Ile Asp
130 135 140

Arg His Phe Gln Asn Glu Ile Arg Val Ala Leu Asp Tyr Val Tyr Ser
145 150 155 160

Tyr Trp Lys Glu Lys Glu Gly Ile Gly Cys Gly Arg Asp Ser Thr Phe
165 170 175

Pro Asp Leu Asn Ser Thr Ala Leu Ala Leu Arg Thr Leu Arg Leu His
180 185 190

Gly Tyr Asn Val Ser Ser Asp Val Leu Glu Tyr Phe Lys Asp Gln Lys
195 200 205

Gly His Phe Ala Cys Pro Ala Ile Leu Thr Glu Gly Gln Ile Thr Arg
210 215 220

Ser Val Leu Asn Leu Tyr Arg Ala Ser Leu Val Ala Phe Pro Gly Glu

225	230	235	240
Lys Val Met Glu Glu Ala Glu Ile Phe Ser Ala Ser Tyr Leu Lys Glu			
245	250	255	
Val Leu Gln Lys Ile Pro Val Ser Ser Phe Ser Arg Glu Ile Glu Tyr			
260	265	270	
Val Leu Glu Tyr Gly Trp His Thr Asn Leu Pro Arg Leu Glu Ala Arg			
275	280	285	
Asn Tyr Ile Asp Val Tyr Gly Gln Asp Ser Tyr Glu Ser Ser Asn Glu			
290	295	300	
Met Pro Tyr Val Asn Thr Gln Lys Leu Leu Lys Leu Ala Lys Leu Glu			
305	310	315	320
Phe Asn Ile Phe His Ser Leu Gln Gln Lys Glu Leu Gln Tyr Ile Ser			
325	330	335	
Arg Trp Trp Lys Asp Ser Cys Ser Ser His Leu Thr Phe Thr Arg His			
340	345	350	
Arg His Val Glu Tyr Tyr Thr Met Ala Ser Cys Ile Ser Met Glu Pro			
355	360	365	
Lys His Ser Ala Phe Arg Leu Gly Phe Val Lys Thr Cys His Leu Leu			
370	375	380	
Thr Val Leu Asp Asp Met Tyr Asp Thr Phe Gly Thr Leu Asp Glu Leu			
385	390	395	400
Gln Leu Phe Thr Thr Ala Phe Lys Arg Trp Asp Leu Ser Glu Thr Lys			
405	410	415	
Cys Leu Pro Glu Tyr Met Lys Ala Val Tyr Met Asp Leu Tyr Gln Cys			
420	425	430	
Leu Asn Glu Leu Ala Gln Glu Ala Glu Lys Thr Gln Gly Arg Asp Thr			
435	440	445	
Leu Asn Tyr Ile Arg Asn Ala Tyr Glu Ser His Phe Asp Ser Phe Met			
450	455	460	
His Glu Ala Lys Trp Ile Ser Ser Gly Tyr Leu Pro Thr Phe Glu Glu			
465	470	475	480
Tyr Leu Lys Asn Gly Lys Val Ser Ser Gly Ser Arg Thr Ala Thr Leu			
485	490	495	
Gln Pro Ile Leu Thr Leu Asp Val Pro Leu Pro Asn Tyr Ile Leu Gln			
500	505	510	
Glu Ile Asp Tyr Pro Ser Arg Phe Asn Asp Leu Ala Ser Ser Leu Leu			
515	520	525	
Arg Leu Arg Gly Asp Thr Arg Cys Tyr Lys Ala Asp Arg Ala Arg Gly			
530	535	540	
Glu Glu Ala Ser Ala Ile Ser Cys Tyr Met Lys Asp His Pro Gly Ser			
545	550	555	560

Thr Glu Glu Asp Ala Leu Asn His Ile Asn Val Met Ile Ser Asp Ala
565 570 575

Ile Arg Glu Leu Asn Trp Glu Leu Leu Arg Pro Asp Ser Lys Ser Pro
580 585 590

Ile Ser Ser Lys Lys His Ala Phe Asp Ile Thr Arg Ala Phe His His
595 600 605

Leu Tyr Lys Tyr Arg Asp Gly Tyr Thr Val Ala Ser Ser Glu Thr Lys
610 615 620

Asn Leu Val Met Lys Thr Val Leu Glu Pro Val Ala Leu
625 630 635

<210> 70

<211> 696

<212> DNA

<213> Abies grandis

<400> 70

gcatttaaga gatgggatcc gtctgccaca gatttgcttc cagagtatat gaaagggttg 60

tacatggtgg tttacgaaac cgtaaatgaa attgctcgag aggcagacaa gtctcaaggc 120

cgagagacgc tcaacgatgc tcgacgagct tgggaggcct atcttgattc gtatataaaa 180

gaagctgagt ggatctccag tggttatctg ccaacgtttg aggagtagat ggagaccaggc 240

aaagtttagtt ttggtttatcg catattcgca ttgcaaccca tcctcactat ggatgttccc 300

cttactcacc acatcctgca ggaaatagac tttccattga ggttaatga cttaatatgt 360

tccatccttc gactaaaaaa tgacactcgcg tgctacaagg cggacaggc ccgtggagaa 420

gaagcttcgt gtatatacgat ttatataaaa gagaatcctg gatcaacaga ggaagatgt 480

atcaatcata tcaacgctat ggtcaataac ttaatcaaag aagtgaatttgg gagcttctc 540

cgacaggacg gcaccgctca tattgcttgc aagaaacacg ctttgacat cctcaaagg 600

tcccttcacg gctacaaata ccgagatggg ttcagcggtt ccaacaagga aaccaagaat 660

tgggtgagga gaacagtcct tgagtctgtt cctttg 696

<210> 71

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
oligonucleotide

<220>

<221> misc_feature

<222> (1)..(20)

<223> Reverse RACE primer 10-2

<400> 71
acgaagcttc ttctccacgg 20

<210> 72
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<220>
<221> misc_feature
<222> (1)..(20)
<223> Reverse RACE primer 10-4

<400> 72
ggatccccatc tcttaactgc 20

<210> 73
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<220>
<221> misc_feature
<222> (1)..(27)
<223> PCR primer AP1

<400> 73
ccatccta atcgactca ataggc 27

<210> 74
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<220>
<221> misc_feature
<222> (1)..(23)
<223> PCR primer AP2

<400> 74
actcactata gggctcgagc ggc 23

<210> 75
<211> 24

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<220>
<221> misc_feature
<222> (1)..(24)
<223> PCR primer AG9F

<400> 75
atggctcttg tttcttatctt gccc 24

<210> 76
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<220>
<221> misc_feature
<222> (1)..(24)
<223> PCR primer AG9R

<400> 76
ttacaaaaggc acagactcaa ggac 24

<210> 77
<211> 1890
<212> DNA
<213> Abies grandis

<220>
<221> CDS
<222> (1)..(1890)

<400> 77
atg gct ctt gtt tct atc ttg ccc ttg tct tcc aaa tcg gtc ctg cac 48
Met Ala Leu Val Ser Ile Leu Pro Leu Ser Ser Lys Ser Val Leu His
1 5 10 15

aaa tcg tgg atc gtt tct act tat gag cat aag gct atc agt aga aca 96
Lys Ser Trp Ile Val Ser Thr Tyr Glu His Lys Ala Ile Ser Arg Thr
20 25 30

atc cca aat ctt gga ttg cgt ggg cga ggg aaa tct gtg aca cat tcc 144
Ile Pro Asn Leu Gly Leu Arg Gly Arg Gly Lys Ser Val Thr His Ser
35 40 45

ctg aga atg agt ttg agc acc gca gtc tct gat gat cat ggt gta caa 192
Leu Arg Met Ser Leu Ser Thr Ala Val Ser Asp Asp His Gly Val Gln
50 55 60

aga cgc ata gtc gag ttt cat tcc aat ctg tgg gac gac gat ttc ata 240

Arg Arg Ile Val Glu Phe His Ser Asn Leu Trp Asp Asp Asp Phe Ile				
65	70	75	80	
caa tct cta tca acg cct tat ggg gca cct tca tac cgt gaa cgt gct				288
Gln Ser Leu Ser Thr Pro Tyr Gly Ala Pro Ser Tyr Arg Glu Arg Ala				
85	90	95		
gat aga ctt att gtg gaa gta aag ggt ata ttc act tca att tca gcg				336
Asp Arg Leu Ile Val Glu Val Lys Gly Ile Phe Thr Ser Ile Ser Ala				
100	105	110		
gaa gat gga gaa cta atc act ccc ctc aat gat ctc att caa cgc ctt				384
Glu Asp Gly Glu Leu Ile Thr Pro Leu Asn Asp Leu Ile Gln Arg Leu				
115	120	125		
tta atg gtc gat aac gtt gaa cgt tta ggg att gat aga cat ttc aaa				432
Leu Met Val Asp Asn Val Glu Arg Leu Gly Ile Asp Arg His Phe Lys				
130	135	140		
aat gag ata aaa gca gca cta gac tat gtt tac agt tat tgg aac gaa				480
Asn Glu Ile Lys Ala Ala Leu Asp Tyr Val Tyr Ser Tyr Trp Asn Glu				
145	150	155	160	
aaa ggc att ggc agt gga agt gat agt ggt gtt gct gat ctc aac tca				528
Lys Gly Ile Gly Ser Gly Ser Asp Ser Gly Val Ala Asp Leu Asn Ser				
165	170	175		
act gcc ctg ggg ttt cga att ctt cga cta cac gga tac agt gtt tct				576
Thr Ala Leu Gly Phe Arg Ile Leu Arg Leu His Gly Tyr Ser Val Ser				
180	185	190		
tca gat gtg ttg gaa cac ttc aaa gag gag aag gag aag ggg cag ttt				624
Ser Asp Val Leu Glu His Phe Lys Glu Glu Lys Glu Lys Gly Gln Phe				
195	200	205		
gta tgt tcg gcc atc caa aca gag gaa gag ata aaa agc gtt ctg aat				672
Val Cys Ser Ala Ile Gln Thr Glu Glu Glu Ile Lys Ser Val Leu Asn				
210	215	220		
tta ttt cgg gcc tcc ctc att gcc ttt cct ggg gag aaa gtt atg gaa				720
Leu Phe Arg Ala Ser Leu Ile Ala Phe Pro Gly Glu Lys Val Met Glu				
225	230	235	240	
gag gct gaa atc ttc tct aaa ata tat tta aaa gaa gcc tta caa aat				768
Glu Ala Glu Ile Phe Ser Lys Ile Tyr Leu Lys Glu Ala Leu Gln Asn				
245	250	255		
att gct gtc tcc agt ctt tca cga gag ata gag tac gtt ctg gag gat				816
Ile Ala Val Ser Ser Leu Ser Arg Glu Ile Glu Tyr Val Leu Glu Asp				
260	265	270		
ggt tgg caa aca aat atg cca aga ttg gaa aca agg aac tac atc gat				864
Gly Trp Gln Thr Asn Met Pro Arg Leu Glu Thr Arg Asn Tyr Ile Asp				
275	280	285		
gta ttg gga gag aac gat cgt gat gag acg tta tat atg aac atg gag				912
Val Leu Gly Glu Asn Asp Arg Asp Glu Thr Leu Tyr Met Asn Met Glu				
290	295	300		
aaa ctt tta gaa att gca aaa ttg gag ttc aat att ttt cac tcc tta				960
Lys Leu Leu Glu Ile Ala Lys Leu Glu Phe Asn Ile Phe His Ser Leu				

305	310	315	320	
caa cag aga gag cta aaa gac ctc tcc aga tgg tgg aaa gat tcg ggt Gln Gln Arg Glu Leu Lys Asp Leu Ser Arg Trp Trp Lys Asp Ser Gly 325 330 335				1008
ttc tct cac ctg aca ttt tct cgg cat cgt cat gtg gaa ttc tac gct Phe Ser His Leu Thr Phe Ser Arg His Arg His Val Glu Phe Tyr Ala 340 345 350				1056
ctg gca tct tgc att gaa act gat cgc aaa cat tcc gga ttc aga ctc Leu Ala Ser Cys Ile Glu Thr Asp Arg Lys His Ser Gly Phe Arg Leu 355 360 365				1104
ggc ttt gcc aaa atg tgt cat ctt atc acg gtt ttg gac gat ata tac Gly Phe Ala Lys Met Cys His Leu Ile Thr Val Leu Asp Asp Ile Tyr 370 375 380				1152
gac acc ttt gga aca atg gag gag ctg gaa ctc ttc act gca gca ttt Asp Thr Phe Gly Thr Met Glu Glu Leu Glu Leu Phe Thr Ala Ala Phe 385 390 395 400				1200
aag aga tgg gat ccg tct gcc aca gat ttg ctt cca gag tat atg aaa Lys Arg Trp Asp Pro Ser Ala Thr Asp Leu Leu Pro Glu Tyr Met Lys 405 410 415				1248
ggg ttg tac atg gtg gtt tac gaa acc gta aat gaa att gct cga gag Gly Leu Tyr Met Val Val Tyr Glu Thr Val Asn Glu Ile Ala Arg Glu 420 425 430				1296
gca gac aag tct caa ggc cga gag acg ctc aac gat gct cga cga gct Ala Asp Lys Ser Gln Gly Arg Glu Thr Leu Asn Asp Ala Arg Arg Ala 435 440 445				1344
tgg gag gcc tat ctt gat tcg tat atg aaa gaa gct gag tgg atc tcc Trp Glu Ala Tyr Leu Asp Ser Tyr Met Lys Glu Ala Glu Trp Ile Ser 450 455 460				1392
agt ggt tat ctg cca acg ttt gag gag tac atg gag acc agc aaa gtt Ser Gly Tyr Leu Pro Thr Phe Glu Glu Tyr Met Glu Thr Ser Lys Val 465 470 475 480				1440
agt ttt ggt tat cgc ata ttc gca ttg caa ccc atc ctc act atg gat Ser Phe Gly Tyr Arg Ile Phe Ala Leu Gln Pro Ile Leu Thr Met Asp 485 490 495				1488
gtt ccc ctt act cac cac atc ctg cag gaa ata gac ttt cca ttg agg Val Pro Leu Thr His His Ile Leu Gln Glu Ile Asp Phe Pro Leu Arg 500 505 510				1536
ttt aat gac tta ata tgt tcc atc ctt cga ctt aaa aat gac act cgc Phe Asn Asp Leu Ile Cys Ser Ile Leu Arg Leu Lys Asn Asp Thr Arg 515 520 525				1584
tgc tac aag gcg gac agg gcc cgt gga gaa gaa gct tcg tgt ata tcg Cys Tyr Lys Ala Asp Arg Ala Arg Gly Glu Glu Ala Ser Cys Ile Ser 530 535 540				1632
tgt tat atg aaa gag aat cct gga tca aca gag gaa gat gct atc aat Cys Tyr Met Lys Glu Asn Pro Gly Ser Thr Glu Glu Asp Ala Ile Asn 545 550 555 560				1680

cat atc aac gct atg gtc aat aac tta atc aaa gaa gtg aat tgg gag	1728	
His Ile Asn Ala Met Val Asn Asn Leu Ile Lys Glu Val Asn Trp Glu		
565	570	575
ctt ctc cga cag gac ggc acc gct cat att gct tgc aag aaa cac gct	1776	
Leu Leu Arg Gln Asp Gly Thr Ala His Ile Ala Cys Lys Lys His Ala		
580	585	590
ttt gac atc ctc aaa ggt tcc ctt cac ggc tac aaa tac cga gat ggg	1824	
Phe Asp Ile Leu Lys Gly Ser Leu His Gly Tyr Lys Tyr Arg Asp Gly		
595	600	605
ttc agc gtt gcc aac aag gaa acc aag aat tgg gtg agg aga aca gtc	1872	
Phe Ser Val Ala Asn Lys Glu Thr Lys Asn Trp Val Arg Arg Thr Val		
610	615	620
ctt gag tct gtg cct ttg	1890	
Leu Glu Ser Val Pro Leu		
625	630	

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Lys Ser Trp Ile Val Ser Thr Tyr Glu His Lys Ala Ile Ser Arg Thr
20 25 30
Ile Pro Asn Leu Gly Leu Arg Gly Arg Gly Lys Ser Val Thr His Ser
35 40 45
Leu Arg Met Ser Leu Ser Thr Ala Val Ser Asp Asp His Gly Val Gln
50 55 60
Arg Arg Ile Val Glu Phe His Ser Asn Leu Trp Asp Asp Asp Phe Ile
65 70 75 80
Gln Ser Leu Ser Thr Pro Tyr Gly Ala Pro Ser Tyr Arg Glu Arg Ala
85 90 95
Asp Arg Leu Ile Val Glu Val Lys Gly Ile Phe Thr Ser Ile Ser Ala
100 105 110
Glu Asp Gly Glu Leu Ile Thr Pro Leu Asn Asp Leu Ile Gln Arg Leu
115 120 125
Leu Met Val Asp Asn Val Glu Arg Leu Gly Ile Asp Arg His Phe Lys
130 135 140
Asn Glu Ile Lys Ala Ala Leu Asp Tyr Val Tyr Ser Tyr Trp Asn Glu
145 150 155 160
Lys Gly Ile Gly Ser Gly Ser Asp Ser Gly Val Ala Asp Leu Asn Ser
165 170 175

Thr Ala Leu Gly Phe Arg Ile Leu Arg Leu His Gly Tyr Ser Val Ser
180 185 190

Ser Asp Val Leu Glu His Phe Lys Glu Glu Lys Glu Lys Gly Gln Phe
195 200 205

Val Cys Ser Ala Ile Gln Thr Glu Glu Glu Ile Lys Ser Val Leu Asn
210 215 220

Leu Phe Arg Ala Ser Leu Ile Ala Phe Pro Gly Glu Lys Val Met Glu
225 230 235 240

Glu Ala Glu Ile Phe Ser Lys Ile Tyr Leu Lys Glu Ala Leu Gln Asn
245 250 255

Ile Ala Val Ser Ser Leu Ser Arg Glu Ile Glu Tyr Val Leu Glu Asp
260 265 270

Gly Trp Gln Thr Asn Met Pro Arg Leu Glu Thr Arg Asn Tyr Ile Asp
275 280 285

Val Leu Gly Glu Asn Asp Arg Asp Glu Thr Leu Tyr Met Asn Met Glu
290 295 300

Lys Leu Leu Glu Ile Ala Lys Leu Glu Phe Asn Ile Phe His Ser Leu
305 310 315 320

Gln Gln Arg Glu Leu Lys Asp Leu Ser Arg Trp Trp Lys Asp Ser Gly
325 330 335

Phe Ser His Leu Thr Phe Ser Arg His Arg His Val Glu Phe Tyr Ala
340 345 350

Leu Ala Ser Cys Ile Glu Thr Asp Arg Lys His Ser Gly Phe Arg Leu
355 360 365

Gly Phe Ala Lys Met Cys His Leu Ile Thr Val Leu Asp Asp Ile Tyr
370 375 380

Asp Thr Phe Gly Thr Met Glu Glu Leu Glu Leu Phe Thr Ala Ala Phe
385 390 395 400

Lys Arg Trp Asp Pro Ser Ala Thr Asp Leu Leu Pro Glu Tyr Met Lys
405 410 415

Gly Leu Tyr Met Val Val Tyr Glu Thr Val Asn Glu Ile Ala Arg Glu
420 425 430

Ala Asp Lys Ser Gln Gly Arg Glu Thr Leu Asn Asp Ala Arg Arg Ala
435 440 445

Trp Glu Ala Tyr Leu Asp Ser Tyr Met Lys Glu Ala Glu Trp Ile Ser
450 455 460

Ser Gly Tyr Leu Pro Thr Phe Glu Glu Tyr Met Glu Thr Ser Lys Val
465 470 475 480

Ser Phe Gly Tyr Arg Ile Phe Ala Leu Gln Pro Ile Leu Thr Met Asp
485 490 495

Val Pro Leu Thr His His Ile Leu Gln Glu Ile Asp Phe Pro Leu Arg

500

505

510

Phe Asn Asp Leu Ile Cys Ser Ile Leu Arg Leu Lys Asn Asp Thr Arg
515 520 525

Cys Tyr Lys Ala Asp Arg Ala Arg Gly Glu Glu Ala Ser Cys Ile Ser
530 535 540

Cys Tyr Met Lys Glu Asn Pro Gly Ser Thr Glu Glu Asp Ala Ile Asn
545 550 555 560

His Ile Asn Ala Met Val Asn Asn Leu Ile Lys Glu Val Asn Trp Glu
565 570 575

Leu Leu Arg Gln Asp Gly Thr Ala His Ile Ala Cys Lys Lys His Ala
580 585 590

Phe Asp Ile Leu Lys Gly Ser Leu His Gly Tyr Lys Tyr Arg Asp Gly
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Phe Ser Val Ala Asn Lys Glu Thr Lys Asn Trp Val Arg Arg Thr Val
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<223> Mutagenesis primer 6eBamHIF

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<210> 80

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<223> Mutagenesis primer 732eNdeIF

<400> 83
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<210> 84
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<400> 85
ctgatagcaa gctcatatgg ctcttctttc          30

<210> 86
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<223> PCR primer 6-BamHI

<400> 87

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29

<210> 88

<211> 30

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29

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<400> 91
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<210> 96
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<400> 101
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<210> 102
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<400> 102
gaagagatgg gaccgcgtcct cgatag                                26

<210> 103
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<400> 103
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<222> (1)..(25)
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<400> 104
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25

<210> 105
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25

<210> 106
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<220>
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<400> 106
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<210> 107
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<220>
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<222> (1)..(25)
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25